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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 04:10:42 ; Search time 1122.55 Seconds

(without alignments)
10188.783 Million cell updates/sec

Title: US-09-963-803-19

Perfect score: 393
Sequence: 1 aagcttgatgcctgcagca.....cacacaactagagatcc 393Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	393	100.0	393	6	AX036753	AX036753 Sequence
2	314	79.9	462	6	AX036754	AX036754 Sequence
3	310	78.9	392	6	AX036755	AX036755 Sequence
4	304.6	77.5	600	6	AX036756	AX036756 Sequence
5	295.6	75.2	9285	6	AX093047	AX093047 Sequence
6	295.6	75.2	15077	6	AX093052	AX093052 Sequence
7	285.2	72.6	472	6	AX036759	AX036759 Sequence
8	214.4	54.6	317	6	AX036737	AX036737 Sequence
9	212.4	54.0	541	6	AX036758	AX036758 Sequence
10	200.4	51.0	348	6	AX036738	AX036738 Sequence
11	196.2	49.9	604	6	AX036757	AX036757 Sequence
12	154.8	39.4	371	6	AX036739	AX036739 Sequence
13	140.8	35.8	301	6	AX036741	AX036741 Sequence
14	140.8	35.8	398	6	AX036740	AX036740 Sequence
15	120.6	30.7	515	6	AX036736	AX036736 Sequence
16	120.6	30.7	515	6	AX088388	AX088388 Sequence
17	120.6	30.7	532	6	AX020243	AX020243 Sequence
18	120.6	30.7	838	6	AX014764	AX014764 Sequence
19	120.6	30.7	853	6	AX088389	AX088389 Sequence
20	120.6	30.7	1036	6	AX014765	AX014765 Sequence
21	120.6	30.7	8159	14	CVU020341	U20341 Cassava vel
22	120.6	30.7	8159	14	CVU59751	U59751 Cassava vel
23	120.6	30.7	8340	6	AX338536	AX338536 Sequence
24	120.6	30.7	12241	6	AX412168	AX412168 Sequence
25	115.8	29.5	593	6	AX088390	AX088390 Sequence
26	115.8	29.5	857	6	AX088391	AX088391 Sequence
27	115.8	29.5	931	6	AX088392	AX088392 Sequence
28	115.4	29.5	931	6	AX088393	AX088393 Sequence
29	115.4	29.4	931	6	AX088393	AX088393 Sequence
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32	80	20.4	243	6	AX036735	AX036735 Sequence
33	77.8	19.8	392	6	AX036755	AX036755 Sequence
34	69.6	17.7	79	6	AX036611	AX036611 Sequence
35	69.6	17.7	79	6	AX036748	AX036748 Sequence
36	69	17.6	259	6	AX036616	AX036616 Sequence
37	69	17.6	296	6	AX036603	AX036603 Sequence
38	62	15.8	62	6	AX036744	AX036744 Sequence
39	60	15.3	60	6	AX036743	AX036743 Sequence
40	58	14.8	63	6	AX036746	AX036746 Sequence
41	58	14.8	80	6	AX103782	AX103782 Sequence
42	58	14.8	236	6	AX103783	AX103783 Sequence
43	58	14.8	299	6	AX103784	AX103784 Sequence
44	58	14.8	332	6	AX103755	AX103755 Sequence
45	58	14.8	472	6	AX103753	AX103753 Sequence

ALIGNMENTS

RESULT 1
AX036753
LOCUS AX036753 393 bp DNA linear PART 16-NOV-2000
DEFINITION Sequence 19 from Patent WO0058485.
ACCESSION AX036753
VERSION AX036753.1 GI:11226262
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 393)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 19 05-OCT-2000;

MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES ; GRUBER VERONIQUE (FR)
SOURCE 1..393
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1162"
Promoter 1..393
BASE COUNT 128 a 75 c 93 g 97 t
ORIGIN

Query Match 100.0%: Score 393; DB 6; Length 393;
Best Local Similarity 100.0%: Pred. No. 1.2e-102;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGCTTGATGCGCTGCAGACATAGTATCCGGCTCATCATGACATCATGACATGACTGA 60
DB 1 AAGCTTGATGCGCTGCAGACATAGTATCCGGCTCATCATGACATCATGACATGACTGA 60
OY 61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGACGTAGACGACGAC 120
DB 61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGACGTAGACGACGAC 120
OY 121 AACATGAAAAGAAAGAAAGTAAAGTCGCGTATTTGAAAAGACATAGAGACATGTA 180
DB 121 AACATGAAAAGAAAGAAAGTAAAGTCGCGTATTTGAAAAGACATAGAGACATGTA 180
OY 181 AGGTGGAATAATGTAAAGGGGGAAGTAACCTTATGATTTGTTGTTGCGACTAGT 240
DB 181 AGGTGGAATAATGTAAAGGGGGAAGTAACCTTATGATTTGTTGTTGCGACTAGT 240
OY 241 GATTGATGTATATCAAGATTGATGTATCTCCACTGACGTAAAGGATGACGATGCC 300
DB 241 GATTGATGTATATCAAGATTGATGTATCTCCACTGACGTAAAGGATGACGATGCC 300
OY 301 ACGTTACCCGGTATGCCGTTTCCCAAGCTTTATTTCTTATTAAAGCACTTGTAGTAG 360
DB 301 ACGTTACCCGGTATGCCGTTTCCCAAGCTTTATTTCTTATTAAAGCACTTGTAGTAG 360
OY 361 CTTAGAAAACCAACACACACACCTTAGAGATCC 393
DB 361 CTTAGAAAACCAACACACACACCTTAGAGATCC 393

RESULT 2
AX036754 462 bp DNA Linear PAT 16-NOV-2000
LOCUS AX036754
DEFINITION Sequence 20 from Patent WO0058485.
ACCESSION AX036754
VERSION AX036754.1 GI:11226263
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 462)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 20 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES ; GRUBER VERONIQUE (FR)
SOURCE 1..462
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1163"
Promoter 1..462
BASE COUNT 148 a 87 c 111 g 116 t
ORIGIN

Query Match 79.9%: Score 314; DB 6; Length 462;
Best Local Similarity 85.1%: Pred. No. 7.7e-80;
Matches 393; Conservative 0; Mismatches 0; Indels 69; Gaps 1;

OY 1 AAGCTTGATGCGCTGCAGACATAGTATCCGGCTCATCATGACATCATGACATGACTGA 60
DB 1 AAGCTTGATGCGCTGCAGACATAGTATCCGGCTCATCATGACATCATGACATGACTGA 60
OY 61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGACGTAGACGACGAC 120
DB 61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGACGTAGACGACGAC 120
OY 121 AACATGAAAAGAAAGAAAGTAAAGTCGCGTATTTGAAAAGACATAGAGACATGTA 180
DB 121 AACATGAAAAGAAAGAAAGTAAAGTCGCGTATTTGAAAAGACATAGAGACATGTA 180
OY 181 AGGTGGAATAATGTAAAGGGGGAAGTAACCTTATGATTTGTTGTTGCGACTAGT 240
DB 181 AGGTGGAATAATGTAAAGGGGGAAGTAACCTTATGATTTGTTGTTGCGACTAGT 240
OY 232 ----- 231
DB 241 GATTGATGTATATCAAGATTGATGTATCTCCACTGACGTAAAGGATGACGATGCC 300
OY 232 ACGATAGATGATGTATGATATCAAGATTGATGTATGATATCCACTGACGTAAAGGATG 291
DB 301 ACGATAGATGATGTATGATATCAAGATTGATGTATGATATCCACTGACGTAAAGGATG 360
OY 292 ACGATGCGACGTTTACCCGGTATGCCGTTTCCCAAGCTTTATTTCTTATTAAAGCACTT 351
DB 361 ACGATGCGACGTTTACCCGGTATGCCGTTTCCCAAGCTTTATTTCTTATTAAAGCACTT 420
OY 352 GTGTAGTAGCTTAAAGAAACCAACACACACACCTTAGAGATCC 393
DB 421 GTGTAGTAGCTTAAAGAAACCAACACACACACCTTAGAGATCC 462

RESULT 3
AX036755 392 bp DNA Linear PAT 16-NOV-2000
LOCUS AX036755
DEFINITION Sequence 21 from Patent WO0058485.
ACCESSION AX036755
VERSION AX036755.1 GI:11226264
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 392)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 21 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES ; GRUBER VERONIQUE (FR)
SOURCE 1..392
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1164"
Promoter 1..392
BASE COUNT 127 a 80 c 87 g 98 t
ORIGIN

Query Match 78.9%: Score 310; DB 6; Length 392;
Best Local Similarity 88.2%: Pred. No. 1.1e-78;
Matches 337; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

OY 1 AAGCTTGATGCGCTGCAGACATAGTATCCGGCTCATCATGACATCATGACATGACTGA 60
DB 1 AAGCTTGATGCGCTGCAGACATAGTATCCGGCTCATCATGACATCATGACATGACTGA 60
OY 61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGACGTAGACGACGAC 120
DB 61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGACGTAGACGACGAC 120
OY 121 AACATGAAAAGAAAGAAAGTAAAGTCGCGTATTTGAAAAGACATAGAGACATGTA 180
DB 121 AACATGAAAAGAAAGAAAGTAAAGTCGCGTATTTGAAAAGACATAGAGACATGTA 180

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Db 121 AACATGAAAAGAAAGATAGTCCGTCGTTGTGAAAAGACATAGAGACATGTA 180
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Qy 181 AGGTGAAAATGTAAGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGT 240
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Db 181 AGGTGAAAATGTAAGGCGGAAAGTAACCTTATGCAATTTGGTTACGAGGAT 240
|||
Qy 241 GATTGATGTATATCAAGATTGATGTATCTCCACTGACGTAAAGGATGACCATGCC 300
|||
Db 241 GCGTCATCCCTTACGTGATGAGATATACATCAATCTTGATATCAATCAATCCTAG 300
|||
Qy 301 ACCTTACCCGGTATGCCGGTCCCAAGCTTATTTCCCTATTTTAAAGACATGTTAGTAGT 360
|||
Db 301 TCGTATACCCGGTATGCCGGTCCCAAGCTTATTTCCCTATTTTAAAGCATTTGTAGTAG 360
|||
Qy 361 CTTAGAAAACCAACACAACAC 382
|||
Db 361 CTTAGAAAACCAACACAACAC 382
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RESULT 4
LOCUS AX036756 600 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 22 from Patent WO0058485.
ACCESSION AX036756
VERSION AX036756.1 GI:11226265
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
JOURNAL mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 22 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
location/Qualifiers
source 1..600
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1165"
BASE COUNT 188 a 111 c 147 g 154 t
ORIGIN
promoter 1..600
BASE COUNT 188 a 111 c 147 g 154 t
ORIGIN

Query Match 77.5%; Score 304.6; DB 6; Length 600;
Best Local Similarity 94.3%; Pred. No. 4e-77;
Matches 316; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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RESULT 5
LOCUS AX093047 9285 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 52 from Patent WO0118192.
ACCESSION AX093047
VERSION AX093047.1 GI:13509522
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gruber,V. and Comeau,D.
TITLE Synthetic vectors, transgenic plants containing them, and methods
JOURNAL for obtaining them
PATENT: WO 0118192-A 52 15-MAR-2001;
MERISTEM THERAPEUTICS (FR)
FEATURES
location/Qualifiers
source 1..9285
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PMR1336"
misc_feature 1
/note="PMR1336 results from the insertion into PMR1196
of the promoter MPr1165 isolated from plasmid PMR1322 as
described in PCT patent application PCT/IB00/00370"
BASE COUNT 2440 a 2252 c 2506 g 2087 t
ORIGIN

Query Match 75.2%; Score 295.6; DB 6; Length 9285;
Best Local Similarity 94.2%; Pred. No. 1.6e-74;
Matches 307; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 10 TGCCTGAGCACTAGTATCCGCCGTCATCATGACATCATCAGTACTGAGAGATGAA 69
|||
Db 5799 TGCCTGAGCACTAGTATCCGCCGTCATCATGACATCATCAGTACTGAGAGATGAA 5858
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Qy 70 TAGCTAGCAGTACACTCTGTGCGAATTTGGAAGACGTAAAGCAGTACGACATGAA 129
|||
Db 5859 TAGCTAGCAGTACACTCTGTGCGAATTTGGAAGACGTAAAGCAGTACGACATGAA 5918
|||
Qy 130 AAGAAGAAATAGGTGGTGGTATGTGAAGAGACATAGAGAGACATAGTAAAGTGA 189
|||
Db 5919 AAGAAGAAATAGGTGGTGGTATGTGAAGAGACATAGAGAGACATAGTAAAGTGA 5978
|||
Qy 190 ATGTAAAGGCGGAAAGTAACTTATGCAATTTGTAATTTGTTACAGTATGATGAT 249
|||
Db 5979 ATGTAAAGGCGGAAAGTAACTTATGCAATTTGTAATTTGTTACAGTATGATGAT 6038
|||
Qy 250 GATATCAAGATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAGTTACC 309
|||
Db 6039 GATATCAAGATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAGTTACC 6098
|||
Qy 310 GGTATGCCGGTTCACAGCTTATTT 335
|||
Db 6099 GATTGATGTATATCAAGATTGATGT 6124
|||

RESULT 6
LOCUS AX093052 15077 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 57 from Patent WO0118192.
ACCESSION AX093052
VERSION AX093052.1 GI:13509527
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gruber,V. and Comeau,D.
TITLE Synthetic vectors, transgenic plants containing them, and methods
for obtaining them
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200 11GHIJGAIHILICCHLIGHCGLAAGBGLIGHCGLHIGLCCALGL 1WCCBBLMIGLCCBL
201

Db 227 -----|||||
-----GTTACCGGTATGCCG 243

Qy 320 TTCCCAAGCTTATTTCTTATTTAAGACCTTGTTAGTACTTATAGAAACCAACACAC 379
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Db 244 TTCCCAAGCTTATTTCTTATTTAAGACCTTGTTAGTACTTATAGAAACCAACACAC 303
|||||

Qy 380 AACCTAGAGATCC 393
|||||
Db 304 AACCTAGAGATCC 317

RESULT 9
AX036758 541 bp DNA linear PAT 16-NOV-2000
LOCUS
DEFINITION Sequence 24 from Patent W0058485.
ACCESSION AX036758
VERSION AX036758.1 GI:11226267
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.

REFERENCE
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 24 05-OCT-2000.
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
LOCATION/Qualifiers
source 1. .541
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1168"

Promoter 1. .541
BASE COUNT 169 a 104 c 130 g 138 t
ORIGIN

Query Match 54.0%; Score 212.4; DB 6; Length 541;
Best Local Similarity 91.5%; Pred. No. 1.7e-50;
Matches 236; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

Qy 78 CATGACACTGTGCGATATTTGAAGACGTAGACAGTGAACAATGAAGAAGAA 137
|||||
Db 160 CATGCCACTGTGCGATATTTGAAGACGTAGACAGTGAACAATGAAGAAGAA 219
|||||

Qy 138 GATAAGTCGGTGTGTTGAAGACATAGAGACATGTAGTGAAGTGAAG 197
|||||
Db 220 GATAAGTCGGTGTGTTG-AAGAGACATAGAGACATGTAGTGAAGTGAAG 278
|||||

Qy 198 GCGAAGTAACTTATGATTTGTAATTGGTTACGACTAGTGAATGATGATTCAA 257
|||||
Db 279 GCGAAGTAACTTATGATTTGTAATTGGTTACGACTAGTGAATGATGATTCAA 338
|||||

Qy 258 GATGATGTGATATCTCCAGTGAAGGATGACGATGCCACGTTACCCGTTATGCC 317
|||||
Db 339 GATGATGTGATATCTCCAGTGAAGGATGACGATGCCACGTTATGCCGTTATGCC 398
|||||

Qy 318 GGTTCACCAAGCTTATTT 335
|||||
Db 399 TGATATCAAGATGATGT 416

RESULT 10
AX036738 348 bp DNA linear PAT 16-NOV-2000
LOCUS
DEFINITION Sequence 4 from Patent W0058485.
ACCESSION AX036738
VERSION AX036738.1 GI:11226247
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 348)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 4 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
LOCATION/Qualifiers
source 1. .348
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1117"

Promoter 1. .348
BASE COUNT 116 a 70 c 78 g 84 t
ORIGIN

Query Match 51.0%; Score 200.4; DB 6; Length 348;
Best Local Similarity 99.1%; Pred. No. 4.9e-47;
Matches 212; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 20 ACTAGTATCCGCGTCATCATATGACATCATCATGACTGAGAGATGATGCTAGCCA 79
|||||
Db 52 ACTAGTATCCGCGTCATCATATGACATCATCATGACTGAGAGATGATGCTAGCCA 111
|||||

Qy 80 TGACACTGTGCGAATATTTGAAGACGTAGACACTGACGACAAATGAAGAAGA 139
|||||
Db 112 TGACACTGTGCGAATATTTGAAGACGTAGACACTGACGACAAATGAAGAAGA 171
|||||

Qy 140 TAACTGCGTGTATTTGAAGACATTAAGACATGTAAGTGAAGTGAAGGCC 199
|||||
Db 172 TAACTGCGTGTATTTG-AAGAGACATTAAGACATGTAAGTGAAGTGAAGGCC 230
|||||

Qy 200 GGAAGTAACTTATGATTTGTAATTGGTTAC 233
|||||
Db 231 GGAAGTAACTTATGATTTGTAATTGGTTAC 264
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RESULT 11
AX036757 604 bp DNA linear PAT 16-NOV-2000
LOCUS
DEFINITION Sequence 23 from Patent W0058485.
ACCESSION AX036757
VERSION AX036757.1 GI:11226266
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 604)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 23 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
LOCATION/Qualifiers
source 1. .604
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1167"

Promoter 1. .604
BASE COUNT 186 a 116 c 145 g 157 t
ORIGIN

Query Match 49.9%; Score 196.2; DB 6; Length 604;
Best Local Similarity 97.4%; Pred. No. 8.1e-46;
Matches 221; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

Qy 78 CATGACACTGTGCGATATTTGAAGACGTAGACAGTGAACAATGAAGAAGAA 137
|||||
Db 160 CATGCCACTGTGCGATATTTGAAGACGTAGACAGTGAACAATGAAGAAGAA 219
|||||

Qy 138 GATAAGTCGGTGTGTTGAAGACATAGAGACATGTAGTGAAGTGAAGTGAAG 197
|||||

Db 220 GATTAAGTGTGATTTGTG-AAGAGACATAGAGACACATGTAAGGTGGAATAATGTAAG 278
 Qy 198 GCGGAAGTAACCTTATGATTTGTAATTTGGTTACAGATGATGATATCA 257
 Db 279 GCGGAAGTAACCTTATGATTTGTAATTTGGTTACAGATGATGATATCA 336
 Qy 258 GATTGATGATATTCACACTGACGTAGAGATGACGATGCCAGCT 304
 Db 337 GATTGATGATATTCACACTGACGTAGAGATGACGATGCCAGCT 383

 RESULT 12
 AX036739 371 bp DNA linear PAT 16-NOV-2000
 LOCUS AX036739
 DEFINITION Sequence 5 from Patent W0058485.
 ACCESSION AX036739
 VERSION AX036739.1 GI:11226248
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 371)
 AUTHORS Range,I., Theisen,M. and Gruber,Y.
 TITLE Chimeric expression promoters originating from commelina yellow
 JOURNAL mottle virus and cassava vein mosaic virus
 Patent: WO 0058485-A 5 05-OCT-2000;
 MERISTEM THERAPEUTICS (FR) ; RANCE INNN (FR) ; THEISEN MANFRED (FR)
 FEATURES
 source location/Qualifiers
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 /db_xref="taxon:32630"
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 promoter 1..371
 BASE COUNT 122 a 68 c 89 g 92 t
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 Query Match 39.4%; Score 154.8; DB 6; Length 371;
 Best Local Similarity 75.9%; Pred. No. 7.3e-34;
 Matches 240; Conservative 0; Mismatches 2; Indels 74; Gaps 1;
 Qy 78 CATGACACTCTGTGCGAATATTGAACGCTAGACGACACAAATGAAGAAGAA 137
 Db 130 CATGCCACTCTGTGCGAATATTGAACGCTAGACGACACAAATGAAGAAGAA 189
 Qy 138 GATTAAGTGTGATTTGTGAAGAGACATAGAGACACATGTAAGGTGGAATAATGTAAG 197
 Db 190 GATTAAGTGTGATTTGTGAAGAGACATAGAGACACATGTAAGGTGGAATAATGTAAG 249
 Qy 198 GCGGAAGTAACCTTATGATTTGTAATTTGGTTACAGATGATGATATCA 257
 Db 250 GCGGAAGTAACCTTATGATTTGTAATTTGGTTACAGATGATGATATCA 280
 Qy 258 GATTGATGATATTCACACTGACGTAGAGATGACGATGCCAGCTTACCGGATGCC 317
 Db 281 -----GTTACCGGATGCC 295
 Qy 318 GATTCCCAAGCTTATTTCTTATTAAGCACTTGTGTAGTACTTGAAGAAACCAACACA 377
 Db 296 GATTCCCAAGCTTATTTCTTATTAAGCACTTGTGTAGTACTTGAAGAAACCAACACA 355
 Qy 378 ACAACCTAGAGATCC 393
 Db 356 ACAACCTAGAGATCC 371

 RESULT 13
 AX036741 301 bp DNA linear PAT 16-NOV-2000
 LOCUS AX036741
 DEFINITION Sequence 7 from Patent W0058485.
 ACCESSION AX036741
 VERSION AX036741.1 GI:11226250
 KEYWORDS

SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 301)
 AUTHORS Range,I., Theisen,M. and Gruber,Y.
 TITLE Chimeric expression promoters originating from commelina yellow
 JOURNAL mottle virus and cassava vein mosaic virus
 Patent: WO 0058485-A 7 05-OCT-2000;
 MERISTEM THERAPEUTICS (FR) ; RANCE INNN (FR) ; THEISEN MANFRED (FR)
 FEATURES
 source location/Qualifiers
 1..301
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="promoter MPr1154"
 promoter 1..301
 BASE COUNT 98 a 54 c 74 g 75 t
 ORIGIN
 Query Match 35.8%; Score 140.8; DB 6; Length 301;
 Best Local Similarity 98.1%; Pred. No. 8.1e-30;
 Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 Qy 78 CATGACACTCTGTGCGAATATTGAACGCTAGACGACACAAATGAAGAAGAA 137
 Db 63 CATGCCACTCTGTGCGAATATTGAACGCTAGACGACACAAATGAAGAAGAA 122
 Qy 138 GATTAAGTGTGATTTGTGAAGAGACATAGAGACACATGTAAGGTGGAATAATGTAAG 197
 Db 123 GATTAAGTGTGATTTGTGAAGAGACATAGAGACACATGTAAGGTGGAATAATGTAAG 181
 Qy 198 GCGGAAGTAACCTTATGATTTGTAATTTGGTTAC 233
 Db 182 GCGGAAGTAACCTTATGATTTGTAATTTGGTTAC 217

 RESULT 14
 AX036740 398 bp DNA linear PAT 16-NOV-2000
 LOCUS AX036740
 DEFINITION Sequence 6 from Patent W0058485.
 ACCESSION AX036740
 VERSION AX036740.1 GI:11226249
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 398)
 AUTHORS Range,I., Theisen,M. and Gruber,Y.
 TITLE Chimeric expression promoters originating from commelina yellow
 JOURNAL mottle virus and cassava vein mosaic virus
 Patent: WO 0058485-A 6 05-OCT-2000;
 MERISTEM THERAPEUTICS (FR) ; RANCE INNN (FR) ; THEISEN MANFRED (FR)
 FEATURES
 source location/Qualifiers
 1..398
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="promoter MPr1147"
 promoter 1..398
 BASE COUNT 128 a 80 c 93 g 97 t
 ORIGIN
 Query Match 35.8%; Score 140.8; DB 6; Length 398;
 Best Local Similarity 98.1%; Pred. No. 8.1e-30;
 Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 Qy 78 CATGACACTCTGTGCGAATATTGAACGCTAGACGACACAAATGAAGAAGAA 137
 Db 160 CATGCCACTCTGTGCGAATATTGAACGCTAGACGACACAAATGAAGAAGAA 219
 Qy 138 GATTAAGTGTGATTTGTGAAGAGACATAGAGACACATGTAAGGTGGAATAATGTAAG 197
 Db 220 GATTAAGTGTGATTTGTG-AAGAGACATAGAGACACATGTAAGGTGGAATAATGTAAG 278

OY 198 GCGGAAGTACCTTATCATTTGTAATTGTTAC 233
 ||||||||||||||||||||||||||||
 Db 279 GCGGAAGTACCTTATCATTTGTAATTGTTAC 314

RESULT 15

AX036736

LOCUS AX036736 515 bp DNA linear PAT 16-NOV-2000

DEFINITION Sequence 2 from Patent WO058485.

ACCESSION AX036736

VERSION AX036736.1 GI:11226245

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 515)

AUTHORS Rance, I., Theisen, M. and Gruber, V.

TITLE Chimeric expression promoters originating from commelina yellow

mottle virus and cassava vein mosaic virus

JOURNAL Patent: WO 0058485-A 2 05-OCT-2000.

MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)

; GRUBER VERONIQUE (FR)

FEATURES

source location/Qualifiers

1..515

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="Promoter from the intergenic region of Cassava Vein

Mosaic Virus of 515 bp in length EMBL U59751"

BASE COUNT 198 a 79 c 109 g 129 t

ORIGIN

Query Match 30.7%; Score 120.6; DB 6; Length 515;
 Best Local Similarity 93.3%; Pred. No. 5.5e-24;
 Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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 |||||

Db 216 GAATCTTGAAAGACGTAGACACTGACGACAAATGAAAGAGAGATAAGTGGTGAT 275
 |||||

OY 153 TGTGAAGAGACATAGACACATGTAGGTGGAATGTAAAGCGCGAAAGTAACCTT 212
 |||||

Db 276 TGTGAAGAGACATAGACACATGTAGGTGGAATGTAAAGCGCGCGAAAGTAACCTT 335
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OY 213 ATGCATTGTAAATT 227
 ||

Db 336 ATCACAAGGAATCT 350
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Search completed: April 14, 2003, 09:29:14
 Job time : 1133.55 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 04:03:41 ; Search time 126.948 Seconds
(without alignments)
6971.612 Million cell updates/sec

Title: us-09-963-803-19

Perfect score: 393
Sequence: 1 aagctgcacgcctgcagca.....cacacaacctagagatcc 393

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	393	100.0	393	21	AAA96853
2	314	79.9	462	21	AAA96854
3	310	78.9	392	21	AAA96855
4	304.6	77.5	600	21	AAA96856
5	285.2	72.6	472	21	AAA96859
6	214.4	54.6	317	21	AAA96837
7	212.4	54.0	341	21	AAA96858
8	200.4	51.0	348	21	AAA96838
9	196.2	49.9	604	21	AAA96857

10	154.8	39.4	371	21	AAA96839	Nucleotide sequenc
11	140.8	35.8	301	21	AAA96841	Nucleotide sequenc
12	140.8	35.8	398	21	AAA96840	Nucleotide sequenc
13	120.6	30.7	392	19	AAV14019	CSVMV promoter CVP
14	120.6	30.7	411	19	AAV14021	CSVMV promoter pb.
15	120.6	30.7	515	21	AAA96836	Promoter from inte
16	120.6	30.7	515	22	AAFE5505	Nucleotide sequenc
17	120.6	30.7	524	19	AAV14020	CSVMV promoter CVP
18	120.6	30.7	526	19	AAV14018	CSVMV promoter pa.
19	120.6	30.7	532	22	AAAD11575	Cassava vein Mosaic
20	120.6	30.7	853	22	AAFE5506	Nucleotide sequenc
21	120.6	30.7	1839	24	ABL57988	4-Hydroxyphenylpyr
22	120.6	30.7	4677	24	ABL57989	4-Hydroxyphenylpyr
23	120.6	30.7	8187	24	ABL58082	4-Hydroxyphenylpyr
24	120.6	30.7	8340	24	ABA04735	Binary vector pAG1

ALIGNMENTS

RESULT 1
ID AAA96853 standard; DNA: 393 BP.
AAA96853:
19-FEB-2001 (first entry)
Nucleotide sequence of chimeric expression promoter MP1162.
Promoter: intergenic region; Commelina yellow mottle virus;
chimeric expression promoter; plant vascular expression promoter;
plant green tissue expression promoter; Cassava vein mosaic virus;
transgenic plant; chimera; ss.
Chimeric - Commelina yellow mottle virus.
Chimeric - Cassava vein mosaic virus.
WO200058485-A1.
05-OCT-2000.
29-MAR-2000; 2000WO-IB00370.
29-MAR-1999; 99FR-0003925.
(MERI-) MERISTEM THERAPEUTICS.
Rance I, Gruber V, Theisen M;
WPI: 2000-647238/62.

PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
PS Claim 5: Page 85; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
XX
SQ Sequence 393 BP; 128 A; 75 C; 93 G; 97 T; 0 other;
XX
XX
Query Match 100.0%; Score 393; DB 21; Length 393;
Best Local Similarity 100.0%; Pred. No. 8e-111;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AACCTTGCAATGCTCGAGCAGCTAGTATCCGCCCTCATCATGACATCATCAGTACTGA 60
DB 1 AACCTTGCAATGCTCGAGCAGCTAGTATCCGCCCTCATCATGACATCATCAGTACTGA 60
OY 61 GGAGATGAATAGCTAGCCTAGACACTCTGTGGCAATATTGAGACGTAAGCACTGACGAC 120
DB 61 GGAGATGAATAGCTAGCCTAGACACTCTGTGGCAATATTGAGACGTAAGCACTGACGAC 120
OY 121 AACATGAAAGAAAGAAATAGTGTGCGTATGTGAAAGAGACATAGAGACATGTA 180
DB 121 AACATGAAAGAAAGAAATAGTGTGCGTATGTGAAAGAGACATAGAGACATGTA 180
OY 181 AGGTGGAATAATGTAAAGGGGGAAGTAACCTTATGCAATTGTAAATTGGTTACGACTAGT 240
DB 181 AGGTGGAATAATGTAAAGGGGGAAGTAACCTTATGCAATTGTAAATTGGTTACGACTAGT 240
OY 241 GATTGATGTGATATCAAGATTTGATATCTCCACTGACGTAAGGATGACGATGCC 300
DB 241 GATTGATGTGATATCAAGATTTGATATCTCCACTGACGTAAGGATGACGATGCC 300
OY 301 ACCTTACCGGATGTGCGGATGCCAAGCTTATTTCTTATTTAAGCACTGTGTAGTAG 360
DB 301 ACCTTACCGGATGTGCGGATGCCAAGCTTATTTCTTATTTAAGCACTGTGTAGTAG 360
OY 361 CTTAGAAACCAACACACAACTAGAGATCC 393
DB 361 CTTAGAAACCAACACACAACTAGAGATCC 393
RESULT 2
AA96854
ID AAA96854 standard; DNA; 462 BP.
XX
XX
AC AAA96854;
XX
XX 19-FEB-2001 (first entry)
XX
XX Nucleotide sequence of chimeric expression promoter MP1163.
DE Promoter: intergenic region; Commelina yellow mottle virus;
XX chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
XX Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200056485-A1.
PN

XX
PD 05-OCT-2000.
XX
XX 29-MAR-2000; 2000MO-1B00370.
PF
XX
XX 29-MAR-1999; 99PR-0003925.
PR
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX
XX Range I, Gruber V, Theisen M;
PI
XX
XX WPI; 2000-647238/62.
DR
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
PS Claim 5: Page 86; 91pp; English.
XX
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
XX
SQ Sequence 462 BP; 148 A; 87 C; 111 G; 116 T; 0 other;
XX
XX
Query Match 79.9%; Score 314; DB 21; Length 462;
Best Local Similarity 85.1%; Pred. No. 1.7e-86;
Matches 393; Conservative 0; Mismatches 0; Indels 69; Gaps 1;
OY 1 AACCTTGCAATGCTCGAGCAGCTAGTATCCGCCCTCATCATGACATCATCAGTACTGA 60
DB 1 AACCTTGCAATGCTCGAGCAGCTAGTATCCGCCCTCATCATGACATCATCAGTACTGA 60
OY 61 GGAGATGAATAGCTAGCCTAGACACTCTGTGGCAATATTGAGACGTAAGCACTGACGAC 120
DB 61 GGAGATGAATAGCTAGCCTAGACACTCTGTGGCAATATTGAGACGTAAGCACTGACGAC 120
OY 121 AACATGAAAGAAAGAAATAGTGTGCGTATGTGAAAGAGACATAGAGACATGTA 180
DB 121 AACATGAAAGAAAGAAATAGTGTGCGTATGTGAAAGAGACATAGAGACATGTA 180
OY 181 AGGTGGAATAATGTAAAGGGGGAAGTAACCTTATGCAATTGTAAATTGGTTACGACTAGT 240
DB 181 AGGTGGAATAATGTAAAGGGGGAAGTAACCTTATGCAATTGTAAATTGGTTACGACTAGT 240
OY 232 ----- 231
DB 241 GATTGATGTGATATCAAGATTTGATATCTCCACTGACGTAAGGATGACGATGCC 300
OY 232 ACGACTAGTATGATATCAAGATTTGATATCTCCACTGACGTAAGGATGACGATGCC 291
DB 301 ACGACTAGTATGATATCAAGATTTGATATCTCCACTGACGTAAGGATGACGATGCC 360
OY 292 ACGACTAGTATGATATCAAGATTTGATATCTCCACTGACGTAAGGATGACGATGCC 351
DB 361 ACGACTAGTATGATATCAAGATTTGATATCTCCACTGACGTAAGGATGACGATGCC 420
OY 352 GTGTAGTACTTAGAAACCAACACAACTAGAGATCC 393
DB 421 GTGTAGTACTTAGAAACCAACACAACTAGAGATCC 462
RESULT 3
AA96855

ID	AAA6855 standard; DNA; 392 BP.	
XX	AAA96855;	
XX		
DT	19-FEB-2001 (first entry)	
XX		
DE	Nucleotide sequence of chimeric expression promoter MPr1164.	
XX		
XX	Promoter; Intergenic region; Commelina yellow mottle virus;	
KW	chimeric expression promoter; plant vascular expression promoter;	
KW	plant green tissue expression promoter; Cassava vein mosaic virus;	
KW	transgenic plant; chimera; ss.	
OS	Chimeric - Commelina yellow mottle virus.	
OS	Chimeric - Cassava vein mosaic virus.	
XX		
XX	MO200058485-A1.	
PD	05-OCT-2000.	
XX		
PF	29-MAR-2000; 2000MO-IB00370.	
XX		
PR	29-MAR-1999; 99FR-0003925.	
XX		
PA	(MERIT-) MERISTEM THERAPEUTICS.	
XX		
P1	Rance I, Gruber V, Theisen M;	
XX		
DR	WPI; 2000-647238/62.	
XX		
PT	Chimeric expression promoter for transgenic plant production, comprises	
PT	sequence from promoter comprising vascular expression region replaced	
PT	with sequence from promoter comprising green tissue expression region	
XX		
PS	Claim 5; Page 86; 91pp; English.	
XX		
CC	The present sequence represents a chimeric promoter of the invention.	
CC	The specification describes chimeric expression promoters. These	
CC	chimeric promoters comprise a nucleic acid sequence which is derived	
CC	from a first plant promoter, in which a plant vascular expression	
CC	promoter region is replaced with a nucleic acid sequence derived from	
CC	a second plant promoter comprising a plant green tissue expression	
CC	promoter region. Preferably, the first plant promoter originates from	
CC	Commelina yellow mottle virus, and the second plant promoter originates	
CC	from the Cassava vein mosaic virus. Especially, the promoters are	
CC	derived from intergenic regions. The chimeric promoters are useful	
CC	for producing transgenic plants.	
XX		
SQ	Sequence 392 BP; 127 A; 80 C; 87 G; 98 T; 0 other;	
	Query Match	78.9%; Score 310; DB 21; Length 392;
	Best Local Similarity	88.2%; Pred. No. 2.6e-85;
	Matches 337; Conservative 0; Mismatches 45; Indels 0; Gaps	
QY	1 AAGCTTGCAATCGCTGCACACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGA	60
DB	1 AAGCTTGCAATCGCTGCACACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGA	60
QY	61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGGAAGACGTAAAGCACTACGAC	120
DB	61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGGAAGACGTAAAGCACTACGAC	120
QY	121 AACCAATGAAAAGAAAGACATTAAGCGCGGTGATTTGGAAGAAGACATAGAGGACACATGTA	180
DB	121 AACCAATGAAAAGAAAGACATTAAGCGCGGTGATTTGGAAGAAGACATAGAGGACACATGTA	180
QY	181 AGGTGAAAATGTAAAGGCGGAAGTAACCTTATGCAATTTGTAAATTGGTTACGACTAGT	240
DB	181 AGGTGAAAATGTAAAGGCGGAAGTAACCTTATGCAATTTGTAAATTGGTTACGCGCAT	240
QY	241 GATTGATGTGATATTCACAGATTGATGTATTCCTCAGTACGCTAAGGATGACGATGCC	300

Db	241	GGGTATCCCTTACGTCAGTGAGATATACATCAATCTTGATATACATCAATACATG	300
Oy	301	ACGTTACCCGGATGCGGGTTCGCCAAGCTTATTTCCATTATTAAAGCACTGTGTAGT	360
Db	301	TGCTTACCGGATGCGGGTTCGCCAAGCTTATTTCCATTATTAAAGCACTGTGTAGT	360
Oy	361	CTTAGAAAAACCAACACAAACAC	382
Db	361	CTTAGAAAAACCAACACAAACAC	382
RESULT 4			
AA	96856		
ID	AAA96856	standard; DNA; 600 BP.	
AC	AAA96856;		
XX	19-FEB-2001	(first entry)	
DT			
XX			
DE		Nucleotide sequence of chimeric expression promoter MPR165.	
XX			
KW		Promoter; intergenic region; Commelina yellow mottle virus;	
KW		chimeric expression promoter; plant vascular expression promoter;	
KW		plant green tissue expression promoter; Cassava vein mosaic virus;	
KW		transgenic plant; chimera; ss.	
XX			
OS		Chimeric - Commelina yellow mottle virus.	
OS		Chimeric - Cassava vein mosaic virus.	
XX		WO200058485-A1.	
PN		05-OCT-2000.	
XX			
PD			
XX		29-MAR-2000; 2000WO-IB00370.	
PF			
XX		29-MAR-1999; 99FR-0003925.	
PR			
XX		(MERI-) MERISTEM THERAPEUTICS.	
PA			
XX			
PI		Rance I, Gruber V, Theisen M;	
XX			
DR		WPI; 2000-647238/62.	
XX			
PT		Chimeric expression promoter for transgenic plant production, comprises	
PT		sequence from promoter comprising vascular expression region replaced	
PT		with sequence from promoter comprising green tissue expression region	
XX			
PS		Claim 5; Page 86-87; 91pp; English.	
XX			
CC		The present sequence represents a chimeric promoter of the invention.	
CC		The specification describes chimeric expression promoters. These	
CC		chimeric promoters comprise a nucleic acid sequence which is derived	
CC		from a first plant promoter, in which a plant vascular expression	
CC		promoter region is replaced with a nucleic acid sequence derived from	
CC		a second plant promoter comprising a plant green tissue expression	
CC		promoter region. Preferably, the first plant promoter originates from	
CC		Commelina yellow mottle virus, and the second plant promoter originates	
CC		from the Cassava vein mosaic virus. Especially, the promoters are	
CC		derived from intergenic regions. The chimeric promoters are useful	
CC		for producing transgenic plants.	
XX			
SO		Sequence 600 BP; 188 A; 111 C; 147 G; 154 T; 0 other;	
Query Match 77.5%; Score 304.6; DB 21; Length 600;			
Best Local Similarity 94.3%; Pred. No. 1.4e-83;			
Matches 316; Conservative 0; Mismatches 19; Indels 0; Gaps			
Oy	1	AAGCTTGATGCGCTGACACAGCTAGTATCGCGCGATCATGAATGACATTCACAGTACGA	60
Db	1	AAGCTTGATGCGCTGACACAGCTAGTATCGCGCGATCATGAATGACATTCACAGTACGA	60
Oy	61	GGAGATGAAATGAGCTATGGACATGACACTCTGTGGATATATTGAAGAGCTAAGCACTACGAC	120

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|||||
Db 61 GGAGATGATAGCTACCATGACACTGTGCGAATATTGAAAGCTAAGCATTGACGAC 120
OY 121 AACAATGAAAGAAAGANTAGGTGCGTATGTAAGAAAGACATAGAGACATGTA 180
Db 121 AACAATGAAAGAAAGANTAGGTGCGTATGTAAGAAAGACATAGAGACATGTA 180
OY 181 AGGTGGAATATGTAAGGCGGAAAGTAACCTTATGCAATTTGATTGTTAGCTAGT 240
Db 181 AGGTGGAATATGTAAGGCGGAAAGTAACCTTATGCAATTTGATTGTTAGCTAGT 240
OY 241 GATTGATGTAATCAAGATTTGATGTAATCTCCACCTGACGTAAGGATGACGATGCC 300
Db 241 GATTGATGTAATCAAGATTTGATGTAATCTCCACCTGACGTAAGGATGACGATGCC 300
OY 301 ACCTTACCGCGTATGCCGCTTCCCAAGCTTATTT 335
Db 301 ACCTTACCGCGTATGCCGCTTCCCAAGCTTATTT 335

```

RESULT 5

AAA96859 standard; DNA; 472 BP.

19-FEB-2001 (first entry)

Nucleotide sequence of chimeric expression promoter MP1169.

Promoter: intergenic region; Commelina yellow mottle virus;
chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
transgenic plant; chimera; ss.

Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000MO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

WPI; 2000-647238/62.

Chimeric expression promoter for transgenic plant production, comprises
sequence from promoter comprising vascular expression region replaced
with sequence from promoter comprising green tissue expression region

Claim 5; Page 88; 91pp; English.

The present sequence represents a chimeric promoter of the invention.
The specification describes chimeric expression promoters. These
chimeric promoters comprise a nucleic acid sequence which is derived
from a first plant promoter, in which a plant vascular expression
promoter region is replaced with a nucleic acid sequence derived from
a second plant promoter comprising a plant green tissue expression
promoter region. Preferably, the first plant promoter originates from
Commelina yellow mottle virus, and the second plant promoter originates
from the Cassava vein mosaic virus. Especially, the promoters are
derived from intergenic regions. The chimeric promoters are useful
for producing transgenic plants.

Sequence 472 BP; 149 A; 92 C; 112 G; 119 T; 0 other;

Query Match 72.6%; Score 285.2; DB 21; Length 472;
Best local similarity 98.1%; Pred. No. 1.2e-77;
Matches 310; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

```

OY 78 CATGACACTCTGTGCAATATTGAAAGCCTAGACACTGACGACATGAAAGAAAGAA 137
Db 160 CATGCCACTCTGTGCAATATTGAAAGCCTAGACACTGACGACATGAAAGAAAGAA 219
OY 138 GATTAAGTGGTGATTTGTGAAAGAGACATAGAGACATGTAAGGTGGAAATGTAAG 197
Db 220 GATTAAGTGGTGATTTGTGAAAGAGACATAGAGACATGTAAGGTGGAAATGTAAG 278
OY 198 GCGGAAGTAACCTTATGCAATTTGATTGTTAGCACTAGTATGATGATTCAA 257
Db 279 GCGGAAGTAACCTTATGCAATTTGATTGTTAGCACTAGTATGATGATTCAA 338
OY 258 GATTGATGTAATCTCCACCTGACGTAAGGATGACGATGCCAGCTTACCGGTATGCC 317
Db 339 GATTGATGTAATCTCCACCTGACGTAAGGATGACGATGCCAGCTTACCGGTATGCC 398
OY 318 GGTTCACCAAGCTTATTTGCTTATTAAGCACTGTGTAGTACGTAAGAAACCAACACA 377
Db 399 GGTTCACCAAGCTTATTTGCTTATTAAGCACTGTGTAGTACGTAAGAAACCAACACA 456
OY 378 ACAACCTAGAGATCC 393
Db 457 ACAACCTAGAGATCC 472

```

RESULT 6

AAA96837 standard; DNA; 317 BP.

19-FEB-2001 (first entry)

Nucleotide sequence of chimeric expression promoter MP1116.

Promoter: intergenic region; Commelina yellow mottle virus;
chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
transgenic plant; chimera; ss.

Chimeric - Commelina yellow mottle virus.

OS Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000MO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

WPI; 2000-647238/62.

Chimeric expression promoter for transgenic plant production, comprises
sequence from promoter comprising vascular expression region replaced
with sequence from promoter comprising green tissue expression region

Claim 5; Page 81; 91pp; English.

The present sequence represents a chimeric promoter of the invention.
The specification describes chimeric expression promoters. These
chimeric promoters comprise a nucleic acid sequence which is derived
from a first plant promoter, in which a plant vascular expression
promoter region is replaced with a nucleic acid sequence derived from

CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.

XX
SQ Sequence 317 BP; 107 A; 61 C; 74 G; 75 T; 0 other:

Query Match 54.6%; Score 214.4; DB 21; Length 317;
Best Local Similarity 79.9%; Pred. No. 6e-56;
Matches 299; Conservative 0; Mismatches 1; Indels 74; Gaps 1;

YY 20 ACTGATATCCGCGCATCATGACATGATCATGAGTGTAGAGGATGATAGCTAGGCCA 79
DB 18 ACTAGTATCCGCGCATCATGACATGATCATGAGTGTAGAGGATGATAGCTAGGCCA 77
YY 80 TGACACTCTGTGCGAATATTTGAAGACGTAGACACTGACGACAAATGAAAAGAAAGA 139
DB 78 TGACACTCTGTGCGAATATTTGAAGACGTAGACACTGACGACAAATGAAAAGAAAGA 137
YY 140 TAAAGTGGGTATTTGTAAAAGACATGAGGACATGTAAAGTGGAAATGTAAAGGC 199
DB 138 TAAAGTGGGTATTTGTAAAAGACATGAGGACATGTAAAGTGGAAATGTAAAGGC 197
YY 200 GGAAGATTAACCTTATGCTTTGTTAATTTGTTAGACTAGTATGATGATCAAGA 259
DB 198 GGAAGATTAACCTTATGCTTTGTTAATTTGTTAGACTAGTATGATGATCAAGA 256
YY 260 TTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCAGCTTACCGGTATGCGG 319
DB 227 -----GTTACCGGTATGCGG 243
YY 320 TTCCCAAGCTTATTTCTTATTTAAGCACTTGTGTAGCTTGAAGAAACCAACACAC 379
DB 244 TTCCCAAGCTTATTTCTTATTTAAGCACTTGTGTAGCTTGAAGAAACCAACACAC 303
YY 380 AACCTAGGATCC 393
DB 304 AACCTAGGATCC 317

RESULT 7

AAA96858
ID AAA96858 standard; DNA: 541 BP.

XX
AC AAA96858;

XX
DT 19-FEB-2001 (first entry)

XX
DE Nucleotide sequence of chimeric expression promoter MPr1168.

XX
KW Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KW plant green tissue expression promoter; Cassava vein mosaic virus;

KW transgenic plant; chimera; ss.

XX
OS Chimeric - Commelina yellow mottle virus.

OS Chimeric - Cassava vein mosaic virus.

XX
PN WO200058485-A1.

XX
PD 05-OCT-2000.

XX
PF 29-MAR-2000; 2000WO-IB00370.

XX
PR 29-MAR-1999; 99FR-0003925.

XX
PA (MERT-) MERISTEM THERAPEUTICS.
XX Rance I, Gruber V, Theisen M;
XX WPI; 2000-647238/62.
XX
DR

XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
PS Claim 5; Page 87-88; 91pp; English.

CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.

XX
SQ Sequence 541 BP; 169 A; 104 C; 130 G; 138 T; 0 other:

Query Match 54.0%; Score 212.4; DB 21; Length 541;
Best Local Similarity 91.5%; Pred. No. 3e-55;
Matches 236; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

YY 78 CATGACACTCTGTGCGAATATTTGAAGACGTAGACACTGACGACAAATGAAAAGAA 137
DB 160 CATGACACTCTGTGCGAATATTTGAAGACGTAGACACTGACGACAAATGAAAAGAA 219
YY 138 GATTAAGTGGGTATTTGTGAAGACATGAGGACATGTAAAGTGGAAATGTAAAG 197
DB 220 GATTAAGTGGGTATTTGTGAAGACATGAGGACATGTAAAGTGGAAATGTAAAG 278
YY 198 GCGGAAGTAACTTATGATTTGTTAATTTGTTAGCACTAGTATGATGATATCA 257
DB 279 GCGGAAGTAACTTATGATTTGTTAATTTGTTAGCACTAGTATGATGATATCA 338
YY 258 GATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCAGTTACCGGTATGCC 317
DB 339 GATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCAGTTACCGGTATGCC 398
YY 318 GGTGCCAAGCTTATTT 335
DB 399 TGATATCAAGATGATGT 416

RESULT 8

AAA96838
ID AAA96838 standard; DNA: 348 BP.

XX
AC AAA96838;

XX
DT 19-FEB-2001 (first entry)

XX
DE Nucleotide sequence of chimeric expression promoter MPr1117.

XX
KW Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KW plant green tissue expression promoter; Cassava vein mosaic virus;

KW transgenic plant; chimera; ss.

XX
OS Chimeric - Commelina yellow mottle virus.

OS Chimeric - Cassava vein mosaic virus.

XX
PN WO200058485-A1.

XX
PD 05-OCT-2000.

XX
PF 29-MAR-2000; 2000WO-IB00370.
XX 29-MAR-1999; 99FR-0003925.
XX
PR
XX

XX	(MERT-) MERISTEM THERAPEUTICS.
PA	Rance I, Gruber V, Theisen M;
PI	MP1; 2000-647238/62.
XX	
DR	Chimeric expression promoter for transgenic plant production, comprises
PT	sequence from promoter comprising vascular expression region replaced
PT	with sequence from promoter comprising green tissue expression region
PT	-
XX	
PS	Claim 5; Page 87; 91pp; English.
XX	
CC	The present sequence represents a chimeric promoter of the invention.
CC	The specification describes chimeric expression promoters. These
CC	chimeric promoters comprise a nucleic acid sequence which is derived
CC	from a first plant promoter, in which a plant vascular expression
CC	promoter region is replaced with a nucleic acid sequence derived from
CC	a second plant promoter comprising a plant green tissue expression
CC	promoter region. Preferably, the first plant promoter originates from
CC	Commelina yellow mottle virus, and the second plant promoter originates
CC	from the Cassava vein mosaic virus. Especially, the promoters are
CC	derived from intergenic regions. The chimeric promoters are useful
CC	for producing transgenic plants.
SQ	Sequence 604 BP; 186 A; 116 C; 145 G; 157 T; 0 other:
Query Match	49.9%; Score 196.2; DB 21; Length 604;
Best Local Similarity	97.4%; Pred. No. 3e-50; Mismatches 221; Conservative 0; Indels 3; Gaps 2;
OY	78 CATGACACTCTGTGCGATATTGAAGACGTAAAGCCTGCAGACAACAATGAAGAAGAA 137
DB	160 CATGCCACTCTGTGCGAATATTGAAGACGTAAAGCCTGCAGACAACAATGAAGAAGAA 219
OY	138 GATAAGTCGGTGATTTGGAAAAGAGACCTTAAGCACATTAAGTGGAAAAATGTAAAG 197
DB	220 GATTAAGTCGGTGATTTGG--AAGAGACCTTAAGGACACATGTAAAGTGGAAAAATGTAAAG 278
OY	198 GCGGAAAGTAACTTATCATTTGTAATTTGGTTACGACTAGTAGTTGATGTATATCA 257
DB	279 GCGGAAGTAACTTATCATTTGTAATTTGGTTAC--CTAGTATGATGTATGTATATCA 336
OY	258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACT 304
DB	337 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACT 383
RESULT 10	
ID	AAA96839 standard; DNA; 371 BP.
AC	AAA96839;
DT	19-FEB-2001 (first entry)
XX	Nucleotide sequence of chimeric expression promoter MP1146.
XX	Promoter; intergenic region; Comelina yellow mottle virus;
KW	chimeric expression promoter; plant vascular expression promoter;
KW	plant green tissue expression promoter; Cassava vein mosaic virus;
KW	transgenic plant; chimera; ss.
OS	Chimeric - Comelina yellow mottle virus.
OS	Chimeric - Cassava vein mosaic virus.
PN	WO200058485-A1.
PD	05-OCT-2000.
PF	29-MAR-2000; 2000MO-IB00370.

PR 29-MAR-1999; 99FR-0003925.
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX
PS Claim 5; Page 81; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 371 BP; 122 A; 68 C; 89 G; 92 T; 0 other;
XX
Query Match 39.4%; Score 154.8; DB 21; Length 371;
Best local Similarity 75.9%; Pred. No. 1.3e-37;
Matches 240; Conservative 0; Mismatches 2; Indels 74; Gaps 1;
XX
OY 78 CATGACACTCTGCGCAATATTGAAGACGTACGACTGACGACAAACAATGAAGAAGAA 137
DB 130 CATGCCACTCTGCGCAATATTGAAGACGTACGACTGACGACAAACAATGAAGAAGAA 189
OY 138 GATAGGTGCGTATGTTGTAAGAGACATAGAGACACATGTAAAGTGAAGTAAAG 197
DB 190 GATAGGTGCGTATGTTGTAAGAGACATAGAGACACATGTAAAGTGAAGTAAAG 249
OY 198 GCGGAAAGTAACCTTATGCACTTTGTAATTTGTTACGACTAGTGTATGATCA 257
DB 250 GCGGAAAGTAACCTTATGCACTTTGTTACTG----- 280
OY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAGCTTACCGGTATGCC 317
DB 281 -----GTTACCGGTATGCC 295
OY 318 GATTCCCAAGCTTATTTCTTATTTTAAGACATTGTGTACTAGCTTGAAGAAACCAACACA 377
DB 296 GATTCCCAAGCTTATTTCTTATTTTAAGACATTGTGTACTAGCTTGAAGAAACCAACACA 355
OY 378 ACAACCTAGAGATCC 393
DB 356 ACAACCTAGAGATCC 371
XX
RESULT 11
AAA96841
ID AAA96841 standard; DNA; 301 BP.
XX
XX AAA96841;
XX
XX 19-FEB-2001 (first entry)
XX
XX Nucleotide sequence of chimeric expression promoter MP1154.
DE
XX
XX Promoter; intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX

OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
XX
XX 05-OCT-2000.
XX
XX 29-MAR-2000; 2000MO-IB00370.
XX
XX 29-MAR-1999; 99FR-0003925.
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI; 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX
PS Claim 5; Page 82; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 301 BP; 98 A; 54 C; 74 G; 75 T; 0 other;
XX
Query Match 35.8%; Score 140.8; DB 21; Length 301;
Best local Similarity 98.1%; Pred. No. 2.5e-33;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
XX
OY 78 CATGACACTCTGCGCAATATTGAAGACGTACGACTGACGACAAACAATGAAGAAGAA 137
DB 63 CATGCCACTCTGCGCAATATTGAAGACGTACGACTGACGACAAACAATGAAGAAGAA 122
OY 138 GATAGGTGCGTATGTTGTAAGAGACATAGAGACACATGTAAAGTGAAGTAAAG 197
DB 123 GATAGGTGCGTATGTTGTTG- AAGAGACATAGAGACACATGTAAAGTGAAGTAAAG 181
OY 198 GCGGAAAGTAACCTTATGCACTTTGTAATTTGTTAC 233
DB 182 GCGGAAAGTAACCTTATGCACTTTGTTACTGTTAC 217
XX
RESULT 12
AAA96840
ID AAA96840 standard; DNA; 398 BP.
XX
XX AAA96840;
XX
XX 19-FEB-2001 (first entry)
XX
XX Nucleotide sequence of chimeric expression promoter MP1147.
DE
XX
XX Promoter; intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
XX Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX

PN WO200058485-A1.
XX
XX 05-OCT-2000.
PD
XX 29-MAR-2000; 2000WO-1B00370.
PF
XX 29-MAR-1999; 99FR-0003925.
PR
XX (MERIT-) MERISTEM THERAPEUTICS.
PA
XX Rance I, Gruber V, Theisen M;
PI
XX WPI; 2000-647238/62.
DR
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5; Page 82; 91pp; English.
PS
XX The present sequence represents a chimeric promoter of the invention,
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Comellina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
CC
SQ Sequence 398 BP; 128 A; 80 C; 93 G; 97 T; 0 other;
XX
XX
XX Query Match 35.8%; Score 140.8; DB 21; Length 398;
Best Local Similarity 98.1%; Pred. No. 2.8e-33;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
OY 78 CATGACACTCTGTGCGAATATTGAAAGCGTAAGCACTGACGACACAAATGAAAGAAGAA 137
DB 160 CATGCCACTCTGTGCGAATATTGAAAGCGTAAGCACTGACGACACAAATGAAAGAAGAA 219
OY 138 GATAAGGTGCGGTATTGTGAAGACATAGAGACACATGTAAAGTGAAAAATGTAAG 197
DB 220 GATAAGGTGCGGTATTGTG-AAAGACATAGAGACACATGTAAAGTGAAAAATGTAAG 278
OY 198 GCGGAAGTAACCTTATGATTTGTAAATTTGCTTAC 233
DB 279 GCGGAAGTAACCTTATGATTTGTAACTTGTAACTTGTAC 314
RESULT 13
AAV14019
ID AAV14019 standard; DNA; 392 BP.
XX
XX AAV14019;
AC
XX
XX 18-JUN-1998 (first entry)
DT
XX
XX CSVWV promoter CVPL.
DE
XX
XX Cassava vein mosaic virus; CSVWV; promoter; cultivated crop;
KW tissue-specific expression control; transgenic plant; ss.
XX
XX Cassava vein mosaic virus.
OS
XX
XX WO9748819-A1.
PN
XX
XX 24-DEC-1997.
PD
XX
XX 20-JUN-1997; 97WO-US10376.
PF
XX

PR 20-JUN-1996; 96US-0020129.
XX
XX (SCRI) SCRIPPS RES INST.
PA
XX
XX Beachy RN, De Kochko A, Fauquet C, Verdaguer B;
PI
XX
XX WPI; 1998-063157/06.
DR
XX
XX Cassava vein mosaic virus promoter - used to express heterologous
PT DNA sequences for producing transgenic plants having altered
PT phenotype(s)
XX
XX Claim 2; Page 74; 115pp; English.
PS
XX This sequence represents a cassava vein mosaic virus promoter, and
CC is a nucleic acid molecule of the invention. The promoter is capable of
CC initiating transcription of an operably linked heterologous nucleic acid
CC sequence in a plant cell. The CSVWV promoters are active in both monocot
CC and dicot plant species, and therefore can be readily applied to a
CC variety of cultivated crops. Although generally constitutive, the
CC derivative promoters include promoters that can regulate expression in a
CC tissue-specific manner, and therefore are useful for controlling
CC expression of heterologous genes in a tissue-specific manner. The
CC promoters can be used for producing transgenic plants with an altered
CC phenotype.
CC
SQ Sequence 392 BP; 154 A; 64 C; 83 G; 91 T; 0 other;
XX
XX
XX Query Match 30.7%; Score 120.6; DB 19; Length 392;
Best Local Similarity 93.3%; Pred. No. 4.5e-27;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 93 GAATATTGAAGACGTAAAGCACTGACGACACAAATGAAAGAAGATTAAGTCGTGAT 152
DB 143 GAATCTTGAAGACGTAAAGCACTGACGACACAAATGAAAGAAGATTAAGTCGTGAT 202
OY 153 TGTGAAGACACATAGAGACACATGTAAAGTGAAATGTAAAGCGGAAATTAACCTT 212
DB 203 TGTGAAGACACATAGAGACACATGTAAAGTGAAATGTAAAGCGGAAATTAACCTT 262
OY 213 ATGCATTGTAAATTT 227
DB 263 ATGCACAAAGCAATCT 277
RESULT 14
AAV14021
ID AAV14021 standard; DNA; 411 BP.
XX
XX AAV14021;
AC
XX
XX 18-JUN-1998 (first entry)
DT
XX
XX CSVWV promoter PB.
DE
XX
XX Cassava vein mosaic virus; CSVWV; promoter; cultivated crop;
KW tissue-specific expression control; transgenic plant; ss.
XX
XX Cassava vein mosaic virus.
OS
XX
XX WO9748819-A1.
PN
XX
XX 24-DEC-1997.
PD
XX
XX 20-JUN-1997; 97WO-US10376.
PF
XX
XX 20-JUN-1996; 96US-0020129.
PR
XX
XX (SCRI) SCRIPPS RES INST.
PA
XX
XX Beachy RN, De Kochko A, Fauquet C, Verdaguer B;
PI
XX
XX WPI; 1998-063157/06.
DR

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:01:47 ; Search time 40.5155 Seconds

(Without alignments)

2974.765 Million cell updates/sec

Title: US-09-963-803-19

Perfect score: 393

Sequence: 1 aagctgcacgcctgcagca.....cacacaactagagatcc 393

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents.NA:*
2: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
7: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.4	11.3	7218	1	US-08-232-463-14
2	39	9.9	439	1	US-08-247-809A-3
3	39	9.9	439	2	US-08-711-728-3
4	39	9.9	446	1	US-08-764-100-23
5	39	9.9	532	3	US-08-042-426-1
6	39	9.9	532	4	US-09-291-238-1
7	39	9.9	532	4	US-09-330-760-1
8	39	9.9	532	4	US-09-328-473-1
9	39	9.9	532	4	US-09-330-737-1
10	39	9.9	532	4	US-09-329-169-1
11	39	9.9	532	4	US-09-330-714A-1
12	39	9.9	532	4	US-09-328-826-1
13	39	9.9	560	3	US-09-042-426-5
14	39	9.9	560	4	US-09-291-238-5
15	39	9.9	560	4	US-09-330-760-5
16	39	9.9	560	4	US-09-328-473-5
17	39	9.9	560	4	US-09-330-737-5
18	39	9.9	560	4	US-09-329-169-5
19	39	9.9	560	4	US-09-330-714A-5
20	39	9.9	560	4	US-09-328-826-5
21	39	9.9	661	4	US-09-027-998A-33
22	39	9.9	793	1	US-08-371-764-1
23	39	9.9	793	4	US-08-897-736-1
24	39	9.9	831	1	US-08-450-834-5
25	39	9.9	950	6	5177308-3
26	39	9.9	978	1	US-08-446-486-31
27	39	9.9	978	1	US-08-463-308-31

28	39	9.9	979	1	US-08-446-486-30	Sequence 30, Appl
29	39	9.9	979	1	US-08-463-308-30	Sequence 30, Appl
30	39	9.9	980	6	5254799-30	Patent No. 5254799
31	39	9.9	1030	1	US-07-936-163-46	Sequence 46, Appl
32	39	9.9	1030	4	US-08-729-601A-43	Sequence 43, Appl
33	39	9.9	1034	4	US-09-363-970-35	Sequence 35, Appl
34	39	9.9	1138	4	US-09-011-151-8	Sequence 8, Appl
35	39	9.9	1138	4	US-09-011-151-9	Sequence 9, Appl
36	39	9.9	1196	4	US-08-729-601A-46	Sequence 46, Appl
37	39	9.9	1279	4	US-09-185-244-2	Sequence 2, Appl
38	39	9.9	1279	4	US-09-471-913-6	Sequence 6, Appl
39	39	9.9	1303	3	US-08-894-440-2	Sequence 2, Appl
40	39	9.9	1303	4	US-09-458-093-2	Sequence 2, Appl
41	39	9.9	1651	3	US-09-065-999-5	Sequence 5, Appl
42	39	9.9	1651	3	US-09-065-999-6	Sequence 6, Appl
43	39	9.9	1722	1	US-08-247-809A-5	Sequence 5, Appl
44	39	9.9	1722	2	US-08-711-728-5	Sequence 5, Appl
45	39	9.9	1829	1	US-07-966-187-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367.
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOXLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
CLASSIFICATION: 435
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
US-08-232-463-14
Query Match 11.3%, Score 44.4, DB 1, Length 7218;

APPLICANT: Goldbach, Robert W.
TITLE OF INVENTION: Improvements in or Relating to Organic
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
FILING DATE:
APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 57737001s, Allen E.
REGISTRATION NUMBER: 34,490
REFERENCE/DOCKET NUMBER: 137-1061
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-3592
TELEFAX: (415) 857-1125
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-764-100-23

Query Match 9.9%; Score 39; DB 1; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTATATCTCCACTGACGTAAAGGATGACGCA 296
|||||
Db 274 GATTGATGTATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 5
US-09-042-426-1
Sequence 1, Application US/09042426
Patent No. 6114608
GENERAL INFORMATION:
APPLICANT: Irvan J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6114608artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426

FILING DATE: March 13, 1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-042-426-1

Query Match 9.9%; Score 39; DB 3; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTATATCTCCACTGACGTAAAGGATGACGCA 296
|||||
Db 274 GATTGATGTATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 6
US-09-291-238-1
Sequence 1, Application US/09291238
Patent No. 6222104
GENERAL INFORMATION:
APPLICANT: Irvan J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6222104artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO

ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-291-238-1

Query Match 9.9%; Score 39; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 296
DB 274 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 312

RESULT 7
US-09-330-760-1

Sequence 1, Application US/09330760
Patent No. 6229075

GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi

TITLE OF INVENTION: DNA Construct Containing Bacillus

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6229075artis Corporation

STREET: 564 Morris Avenue

CITY: Summit

STATE: New Jersey

COUNTRY: USA

ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/330,760

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/042,426

FILING DATE: March 13, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Hoxie, Thomas

REGISTRATION NUMBER: 32,993

REFERENCE/DOCKET NUMBER: 135/1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8614

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 532 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

IMMEDIATE SOURCE:

CLONE: 35S Promoter

US-09-330-760-1

Query Match 9.9%; Score 39; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 296
DB 274 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 312

RESULT 8
US-09-328-473-1

Sequence 1, Application US/09328473

Patent No. 6232533
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6232533artis Corporation

STREET: 564 Morris Avenue

CITY: Summit

STATE: New Jersey

COUNTRY: USA

ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/328,473

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/042,426

FILING DATE: March 13, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Hoxie, Thomas

REGISTRATION NUMBER: 32,993

REFERENCE/DOCKET NUMBER: 135/1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8614

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 532 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

IMMEDIATE SOURCE:

CLONE: 35S Promoter

US-09-328-473-1

Query Match 9.9%; Score 39; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 296
DB 274 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 312

RESULT 9
US-09-330-737-1

Sequence 1, Application US/09330737
Patent No. 6232534

GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi

TITLE OF INVENTION: DNA Construct Containing Bacillus

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6232534artis Corporation

STREET: 564 Morris Avenue

CITY: Summit

STATE: New Jersey

COUNTRY: USA

ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
Db 274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 12

US-09-328-826-1
Sequence 1, Application US/09328826
Patent No. 6399860

GENERAL INFORMATION:

APPLICANT: Irvlin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6399860artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
ZIP: 07901
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,826
FILING DATE: 09-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DNA (genomic)
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-328-826-1

Query Match 9.9%; Score 39; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
Db 274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 13

US-09-042-426-5
Sequence 5, Application US/09042426
Patent No. 6114608

GENERAL INFORMATION:
APPLICANT: Irvlin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6114608artis Corporation
STREET: 564 Morris Avenue

CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-042-426-5

Query Match 9.9%; Score 39; DB 3; Length 560;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
Db 322 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 360

RESULT 14

US-09-291-238-5
Sequence 5, Application US/09291238
Patent No. 6222104

GENERAL INFORMATION:
APPLICANT: Irvlin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6222104artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-291-238-5

Query Match 9.9%; Score 39; DB 4; Length 560;
Best local Similarity 100.0%; Pred. No. 0.0081;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 296
|||||
DB 322 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 360

RESULT 15

US-09-330-760-5
Sequence 5, Application US/09330760
Patent No. 6229075
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 622907sartis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-330-760-5

Query Match

9.9%; Score 39; DB 4; Length 560;

Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 296
|||||
DB 322 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 360

Search completed: April 14, 2003, 10:28:30
Job time : 47.515 secs

GenCore version 5.1.4.P5_A578
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:29:46 ; Search time 47.268 Seconds
(without alignments) 7293.024 Million cell updates/sec

Title: US-09-963-803-19
Perfect score: 393
Sequence: 1 aagcttgcatgcctgcagca.....cacacaacactagagatcc 393

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpna/US06_NEM_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEM_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	314	79.9	462	9	US-09-963-803-20
3	310	78.9	392	9	US-09-963-803-21
4	304.6	77.5	600	9	US-09-963-803-22
5	285.2	72.6	472	9	US-09-963-803-25
6	212.4	54.6	317	9	US-09-963-803-3
7	212.4	54.0	541	9	US-09-963-803-24
8	200.4	51.0	348	9	US-09-963-803-4
9	196.2	49.9	604	9	US-09-963-803-23
10	154.8	39.4	371	9	US-09-963-803-5
11	140.8	35.8	301	9	US-09-963-803-7
12	140.8	35.8	398	9	US-09-963-803-6
13	120.6	30.7	515	9	US-09-963-803-2
14	120.6	30.7	532	9	US-09-765-555-1
15	120.6	30.7	8340	10	US-09-847-057-4
16	120.6	30.7	8340	10	US-09-874-926-4
17	120.6	30.7	12241	12	US-10-033-190-5
18	80	20.4	243	9	US-09-963-803-1
19	77.8	19.8	392	9	US-09-963-803-21

20	69.6	17.7	79	9	US-09-963-803-14	Sequence 14, Appl
21	62	15.8	62	9	US-09-963-803-10	Sequence 10, Appl
22	60	15.3	60	9	US-09-963-803-9	Sequence 9, Appl1
23	60	15.3	63	9	US-09-963-803-12	Sequence 12, Appl
24	58	14.8	80	10	US-09-870-375-34	Sequence 34, Appl
25	58	14.8	236	10	US-09-870-375-35	Sequence 35, Appl
26	58	14.8	299	10	US-09-870-375-36	Sequence 36, Appl
27	58	14.8	332	10	US-09-870-375-7	Sequence 7, Appl1
28	58	14.8	472	10	US-09-870-375-5	Sequence 5, Appl1
29	55	14.0	65	9	US-09-963-803-8	Sequence 8, Appl1
30	55	14.0	80	10	US-09-870-375-28	Sequence 28, Appl
31	45	11.5	63	9	US-09-963-803-13	Sequence 13, Appl
32	39.2	10.0	63	10	US-09-870-375-33	Sequence 33, Appl
33	39.2	10.0	219	10	US-09-870-375-8	Sequence 8, Appl1
34	39.2	10.0	282	10	US-09-870-375-9	Sequence 9, Appl1
35	39.2	10.0	315	10	US-09-870-375-10	Sequence 10, Appl
36	39.2	10.0	381	10	US-09-870-375-15	Sequence 15, Appl
37	39.2	10.0	455	10	US-09-870-375-6	Sequence 6, Appl1
38	39.2	10.0	505	10	US-09-870-375-11	Sequence 11, Appl
39	39	9.9	566	10	US-09-951-470-3	Sequence 3, Appl1
40	39	9.9	661	10	US-09-943-692-33	Sequence 33, Appl
41	39	9.9	700	9	US-10-138-221-9	Sequence 9, Appl1
42	39	9.9	763	9	US-10-162-214-9	Sequence 9, Appl1
43	39	9.9	3983	10	US-09-758-987-1	Sequence 1, Appl1
44	39	9.9	4973	9	US-09-990-659A-15	Sequence 15, Appl
45	39	9.9	5767	9	US-09-810-861B-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-963-803-19
; Sequence 19, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yell
; FILE REFERENCE: 18433042
; CURRENT APPLICATION NUMBER: US/09/963, 803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCR 1B00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1162
; NAME/KEY: promoter
; LOCATION: (1)..(393)
; OTHER INFORMATION:
US-09-963-803-19
Query Match 100.0%: Score 393; DB 9; Length 393;
Best Local Similarity 100.0%: Pred. No. 2.1e-109;
Matches 393: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGCTTGATGCTGCTGACACTAGTATCCGCGTATCAATGACATCATCAGTACTGA 60
Db 1 AAGCTTGATGCTGCTGACACTAGTATCCGCGTATCAATGACATCATCAGTACTGA 60
OY 61 GGAGTGAATGCTGCTGACACTGCTGCGAATATTGAAGACGTAAAGCATGACGAC 120
Db 61 GGAGTGAATGCTGCTGACACTGCTGCGAATATTGAAGACGTAAAGCATGACGAC 120
OY 121 AACATGAAGAAGAACATATAAGTGGTGAATTGGAAAGACACTAAGGACACATGTA 180

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Db 121 AACAAATGAAAGAAAGATAGAGTGTGATGTGAAAGAGACATAGAGACACATGTA 180
QY 181 AGGTGGAATGTAAAGGGGGAAGTAACCTTATGATGATTTGTAATTTGGTTAGACTAGT 240
Db 181 AGGTGGAATGTAAAGGGGGAAGTAACCTTATGATGATTTGTAATTTGGTTAGACTAGT 240
QY 241 GATTGATGTGATTCAGATTTGATGTGATTCACACTGACGTAAAGGATGACGATGCC 300
Db 241 GATTGATGTGATTCAGATTTGATGTGATTCACACTGACGTAAAGGATGACGATGCC 300
QY 301 ACCTTACCCGGTATGCCGGTCCCAAGCTTATTTCTTATTTAAGCACTTGTGTAGTAG 360
Db 301 ACCTTACCCGGTATGCCGGTCCCAAGCTTATTTCTTATTTAAGCACTTGTGTAGTAG 360
QY 361 CTTAGAAACCAACACACAACTAGAGATCC 393
Db 361 CTTAGAAACCAACACACAACTAGAGATCC 393
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RESULT 2

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US-09-963-803-20
; Sequence 20, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow fl
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIORITY FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIORITY FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIORITY FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1163
; NAME/KEY: promoter
; LOCATION: (1)..(462)
; OTHER INFORMATION:
US-09-963-803-20
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Query Match 79.9%; Score 314; DB 9; Length 462;

Best Local Similarity 85.1%; Pred. No. 1.9e-85;

Matches 393; Conservative 0; Mismatches 0; Indels 69; Gaps 1;

```
QY 1 AACCTTGCAATGCTGACGACACTAGTATCCGCCCTCATCATGATGATCATCATGATGTA 60
Db 1 AACCTTGCAATGCTGACGACACTAGTATCCGCCCTCATCATGATGATGATGATGATGTA 60
QY 61 GGAGATGAATAGCTAGCATGACACTCTGTGCGAATATTGAAGACGTAAAGCATGACGAC 120
Db 61 GGAGATGAATAGCTAGCATGACACTCTGTGCGAATATTGAAGACGTAAAGCATGACGAC 120
QY 121 AACCAATGAAAGAAAGATAGAGTGTGATTTGTAAGAGACATAGAGACATGTA 180
Db 121 AACCAATGAAAGAAAGATAGAGTGTGATTTGTAAGAGACATAGAGACATGTA 180
QY 181 AGGTGGAATGTAAAGGGGGAAGTAACCTTATGATGATTTGTAATTTGGTT 231
Db 181 AGGTGGAATGTAAAGGGGGAAGTAACCTTATGATGATTTGTAATTTGGTTAGACTAGT 240
QY 232 ----- 231
Db 241 GATTGATGTGATTCAGATTTGATGTGATTCACACTGACGTAAAGGATGACGATGCC 300
```

```
QY 232 ACAGTAGTATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 291
Db 301 ACAGTAGTATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 292 ACCGATGCCACGTTACCCGGTATGCCGGTCCCAAGCTTATTTCTTATTTAAGCACTT 351
Db 361 ACCGATGCCACGTTACCCGGTATGCCGGTCCCAAGCTTATTTCTTATTTAAGCACTT 420
QY 352 GTGTAGTACCTTGAAGAAACCAACACAACTAGAGATCC 393
Db 421 GTGTAGTACCTTGAAGAAACCAACACAACTAGAGATCC 462
```

RESULT 3

```
US-09-963-803-21
; Sequence 21, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow fl
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIORITY FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIORITY FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIORITY FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1164
; NAME/KEY: promoter
; LOCATION: (1)..(392)
; OTHER INFORMATION:
US-09-963-803-21
```

Query Match 78.9%; Score 310; DB 9; Length 392;

Best Local Similarity 88.2%; Pred. No. 2.9e-84;

Matches 337; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

```
QY 1 AACCTTGCAATGCTGACGACACTAGTATCCGCCCTCATCATGATGATGATGATGATGATG 60
Db 1 AACCTTGCAATGCTGACGACACTAGTATCCGCCCTCATCATGATGATGATGATGATGATGATG 60
QY 61 GGAGATGAATAGCTAGCATGACACTCTGTGCGAATATTGAAGACGTAAAGCATGACGAC 120
Db 61 GGAGATGAATAGCTAGCATGACACTCTGTGCGAATATTGAAGACGTAAAGCATGACGAC 120
QY 121 AACCAATGAAAGAAAGATAGAGTGTGATTTGTAAGAGACATAGAGACATGTA 180
Db 121 AACCAATGAAAGAAAGATAGAGTGTGATTTGTAAGAGACATAGAGACATGTA 180
QY 181 AGGTGGAATGTAAAGGGGGAAGTAACCTTATGATGATTTGTAATTTGGTTAGACTAGT 240
Db 181 AGGTGGAATGTAAAGGGGGAAGTAACCTTATGATGATTTGTAATTTGGTTAGACTAGT 240
QY 241 GATTGATGTGATTCAGATTTGATGTGATTCACACTGACGTAAAGGATGACGATGCC 300
Db 241 GATTGATGTGATTCAGATTTGATGTGATTCACACTGACGTAAAGGATGACGATGCC 300
QY 301 ACCTTACCCGGTATGCCGGTCCCAAGCTTATTTCTTATTTAAGCACTTGTGTAGTAG 360
Db 301 ACCTTACCCGGTATGCCGGTCCCAAGCTTATTTCTTATTTAAGCACTTGTGTAGTAG 360
QY 361 CTTAGAAACCAACACACAACTAGAGATCC 382
Db 361 CTTAGAAACCAACACACAACTAGAGATCC 382
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```
RESULT 4
US-09-963-803-22
; Sequence 22, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE OF INVENTION: vitus and cassava vein mosaic vitus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1165
; NAME/KEY: promoter
; LOCATION: (1)..(600)
; OTHER INFORMATION:
US-09-963-803-22
```

```
Query Match          77.5%; Score 304.6; DB 9; Length 600;
Best Local Similarity 94.3%; Pred. No. 1.5e-82;
Matches 316; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
```

```
QY 1 AACCTGCATGCTGCAGCACTAGTATCCCGTCATCATGATCATCATCATGATGTA 60
Db 1 AACCTGCATGCTGCAGCACTAGTATCCCGTCATCATGATCATCATCATGATGTA 60
QY 61 GGAGATGAATAGTAGCCATGACACTCTGTGCGAATATTGAAGACGTAAACCTGAC 120
Db 61 GGAGATGAATAGTAGCCATGACACTCTGTGCGAATATTGAAGACGTAAACCTGAC 120
QY 121 AACATGAAAAGAAAGAAAGATAGGTGCGTATGTGAAAAGACATAGAGACATGTA 180
Db 121 AACATGAAAAGAAAGAAAGATAGGTGCGTATGTGAAAAGACATAGAGACATGTA 180
QY 181 AGGTGAAAATGTAAGGCGGAAAGTAACTTATGCTTATGTTGTTAGACTAGT 240
Db 181 AGGTGAAAATGTAAGGCGGAAAGTAACTTATGCTTATGTTGTTAGACTAGT 240
QY 241 GATTGATGATATCAAGATTTGATATCTCCACTGACGTAAAGGATGAGCGATGCC 300
Db 241 GATTGATGATATCAAGATTTGATATCTCCACTGACGTAAAGGATGAGCGATGCC 300
QY 301 ACCTTACCCGGTATGCCGGTTCCCAAGCTTTATTT 335
Db 301 ACCTTACCCGGTATGCCGGTTCCCAAGCTTTATTT 335
QY 301 ACAGTAGTATGATGTATATCAAGATTTGATATCTCCACTGACGTAAAGGATGAGCGATGCC 335
Db 301 ACAGTAGTATGATGTATATCAAGATTTGATATCTCCACTGACGTAAAGGATGAGCGATGCC 335
```

```
RESULT 5
US-09-963-803-25
; Sequence 25, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE OF INVENTION: vitus and cassava vein mosaic vitus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
```

```
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1169
; NAME/KEY: promoter
; LOCATION: (1)..(472)
; OTHER INFORMATION:
US-09-963-803-25
```

```
Query Match          72.6%; Score 285.2; DB 9; Length 472;
Best Local Similarity 98.1%; Pred. No. 1e-76;
Matches 310; Conservative 0; Mismatches 3; Indels 3; Gaps 2;
```

```
QY 78 CATGACACTCTGTGCCAATTTTGAAGACGTAAAGCACTGACGACACATGAAAAGAA 137
Db 160 CATGCCACTCTGTGCCAATTTTGAAGACGTAAAGCACTGACGACACATGAAAAGAA 219
QY 138 GATAGGTGGTGTATGTGAAAGACATAGAGACACATGTAAGTGGAAATGTAAG 197
Db 220 GATAGGTGGTGTATGTGAAAGACATAGAGACACATGTAAGTGGAAATGTAAG 278
QY 198 GCGGAAAGTAACTTATGCAATTTTGAATTTGTTAGCACTGATGATGATATCAA 257
Db 279 GCGGAAAGTAACTTATGCAATTTTGAATTTGTTAGCACTGATGATGATATCAA 338
QY 258 GATTGATGATATCTCCACTGACGTAAAGGATGAGCATGCCAGTTACCGGTATGCC 317
Db 339 GATTGATGATATCTCCACTGACGTAAAGGATGAGCATGCCAGTTACCGGTATGCC 398
QY 318 GGTTCCTCAACTTATTTCTTTTAAAGCACTTGTGTACTTATGAAAACCAACACA 377
Db 399 GGTTCCTCAACTTATTTCTTTTAA--ACTTGTGTACTTATGAAAACCAACACA 456
QY 378 ACAACCTAGAGATGCC 393
Db 457 ACAACCTAGAGATGCC 472
```

```
RESULT 6
US-09-963-803-3
; Sequence 3, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE OF INVENTION: vitus and cassava vein mosaic vitus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 317
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter MPr1116
; NAME/KEY: promoter
; LOCATION: (1)..(317)
; OTHER INFORMATION:
US-09-963-803-3
```

Query Match 54.6%; Score 214.4; DB 9; Length 317;
Best Local Similarity 79.9%; Pred. No. 2.5e-55;
Matches 299; Conservative 0; Mismatches 1; Indels 74; Gaps 1;

```
OY 20 ACTAGTATCCGGCGTCATCATGACATCATCAGTACTGAGAGATGATAGTACCCA 79
DB 18 ACTAGTATCCGGCGTCATCATGACATCATCAGTACTGAGAGATGATAGTACCCA 77
OY 80 TGACACTCTGTGCGAATATTGAAGAGCTAGACCTGACACAAATGAAGAAGAGA 139
DB 78 TGACACTCTGTGCGAATATTGAAGAGCTAGACCTGACACAAATGAAGAAGAGA 137
OY 140 TAAGTCGGTGTATGTGAAGAGACATAGAGACATGTAAGTGAATAATGAAGGC 199
DB 138 TAAGTCGGTGTATGTGAAGAGACATAGAGACATGTAAGTGAATAATGAAGGC 197
OY 200 GGAAGTAACCTTATGATGATTTGTAATTTGGTTACGACTAGTATGATATCACA 259
DB 198 GGAAGTAACCTTATGATGATTTGTAATTTGGTTACGACTAGTATGATATCACA 257
OY 260 TGATGTGATATCTCCACTGACGTAAAGGATGATGATGATGATGATGATGATG 319
DB 227 TGATGTGATATCTCCACTGACGTAAAGGATGATGATGATGATGATGATGATG 226
OY 320 TTCCCAAGCTTATTTCTTATTTAAGCAGCTGTGTAGTACTTGAAGAAACCAACA 379
DB 244 TTCCCAAGCTTATTTCTTATTTAAGCAGCTGTGTAGTACTTGAAGAAACCAACA 303
OY 380 AACCTAGAGATCC 393
DB 304 AACCTAGAGATCC 317
```

RESULT 7

```
US-09-963-803-24
; Sequence 24, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter Mpr1168
; NAME/KEY: promoter
; LOCATION: (1)..(541)
; OTHER INFORMATION:
US-09-963-803-24
```

Query Match 54.0%; Score 212.4; DB 9; Length 541;
Best Local Similarity 91.5%; Pred. No. 1.3e-54;
Matches 236; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

```
OY 78 CATGACACTCTGTGCGAATATTGAAGAGCTAGACCTGACGACAAATGAAGAAGAA 137
DB 160 CATGACACTCTGTGCGAATATTGAAGAGCTAGACCTGACGACAAATGAAGAAGAA 219
OY 138 GATAAGTCGGTGTATGTGAAGAGACATAGAGACATGTAAGTGAATAATGAAG 197
```

```
DB 220 GATAAGTCGGTGTATGTG-AAAGACATAGAGACACATGTAAGTGAATAATGAAG 278
OY 198 GCGGAATTAACCTTATGATTTGTAATTTGGTTACGACTAGTATGATGATATCAA 257
DB 279 GCGGAATTAACCTTATGATTTGTAATTTGGTTACGACTAGTATGATGATATCAA 338
OY 258 GATTGATGTATATCTCCACTGACGTAAAGGATGATGATGATGATGATGATGATG 317
DB 339 GATTGATGTATATCTCCACTGACGTAAAGGATGATGATGATGATGATGATGATG 398
OY 318 GGTCCCAAGCTTATTT 335
DB 399 TGATATCAAGATTGATGT 416
```

RESULT 8

```
US-09-963-803-4
; Sequence 4, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter Mpr1117
; NAME/KEY: promoter
; LOCATION: (1)..(348)
; OTHER INFORMATION:
US-09-963-803-4
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Query Match 51.0%; Score 200.4; DB 9; Length 348;
Best Local Similarity 99.1%; Pred. No. 4.5e-51;
Matches 212; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
OY 20 ACTAGTATCCGGCGTCATCATGACATCATCAGTACTGAGAGATGATAGTACCCA 79
DB 52 ACTAGTATCCGGCGTCATCATGACATCATCAGTACTGAGAGATGATAGTACCCA 111
OY 80 TGACACTCTGTGCGAATATTGAAGAGCTAGACCTGACGACAAATGAAGAAGAGA 139
DB 112 TGACACTCTGTGCGAATATTGAAGAGCTAGACCTGACGACAAATGAAGAAGAGA 171
OY 140 TAAGTCGGTGTATGTGAAGAGACATAGAGACATGTAAGTGAATAATGAAGGC 199
DB 172 TAAGTCGGTGTATGTG-AAAGACATAGAGAGACATGTAAGTGAATAATGAAGGC 230
OY 200 GGAAGTAACCTTATGATGATTTGTAATTTGGTTAC 233
DB 231 GGAAGTAACCTTATGATGATTTGTAATTTGGTTAC 264
```

RESULT 9

```
US-09-963-803-23
; Sequence 23, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: virus and cassava vein mosaic virus
```

Query Match	39.4%;	Score 154.8;	DB 9;	Length 371;
Best Local Similarity	75.9%;	Pred. NO. 3.1e-37;		

Qy	78	CATACACCTCTGTGCGAATATTGGAAGACGTAAAGCAGCAGACACAACATGAAAGAGAA	137
Db	63	CATGCCACTCTGTGCGAATATTGGAAGACGTAAAGCAGCAGACACAACATGAAAGAGAA	122
Qy	138	GATTAAGTCGGTGATTGTTGGAAGACACATAGAGACACATCTAAGTGTGAAAAATGAAG	197
Db	123	GATTAAAGTCGGTGATTGTG -AAGAGACATTAAGGACATCTTAAGTGTGAAAAATGAAG	181
Qy	198	GCGGAAAGTAACCTTATGCATTTGTGTAATTTGGTTAC	233
Db	182	GCGGAAAGTAACCTTATGCATTTGTGTAACCTTGGTTAC	217

Query Match	Similarity	35.8%	Score	140.8	DB	9	Length	398	
Best Local	Similarity	98.1%	Pred.	No. 5.5e-33					
Matches	153	Conservative	0	Mismatches	2	Indels	1	Gaps	1
OY	78	CATGCACTCTGTGGCAATATTGAAGACGTAGACACTGACGACAACAAATGAAGAAGAA	137						
Db	160	CATGCACTCTGTGGCAATATTGAAGACGTAGACACTGACGACAACAAATGAAGAAGAA	219						
OY	138	GATAGGTCGGTGATGTTGGAAGAGACATAGAGACACATGTAAGGTGAAATGTAAAG	197						
Db	220	GATAGGTCGGTGATGTTGTC - AAGACACATAGAGGACACATCTTAAGGTGAAATGTAAAG	278						
OY	198	GCGGAAGTAACTTATGCATTTGTAATTTGGTTAC	233						
Db	279	GCGGAAGTAACTTATGCATTTGTAATTTGGTTAC	314						

```

: OTHER INFORMATION:
US-09-963-803-2

Query Match          30.7%; Score 120.6; DB 9; Length 515;
Best Local Similarity 93.3%; Pred. No. 8.3e-27;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATTTGAAACGCGTAACCACTGACGACACAAATGAAAGAAAGAAAGATTAAGTCGGTGAT 152
Db 216 GAATCTTGAAGACGTAACCACTGACGACACAAATGAAAGAAAGATTAAGTCGGTGAT 275
QY 153 TGTGAAAGAGACATTAAGAGACACATGTAAGGTGGAATAATGTAAGGCGCGAAAGTAACCTT 212
Db 276 TGTGAAAGAGACATTAAGAGACACATGTAAGGTGGAATAATGTAAGGCGCGAAAGTAACCTT 335
QY 213 ATGCATTTGTAATTT 227
Db 336 ATCACAAAGGAATCT 350

RESULT 14
US-09-765-555-1
; Sequence 1, Application US/09765555
; Publication No. US20030037355A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: Methods and compositions to modulate
FILE OF INVENTION: expression in plants
FILE REFERENCE: 27801-20014.40
CURRENT APPLICATION NUMBER: US/09/765,555
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 09/620,897
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,468
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 532
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter CSMV
US-09-765-555-1

Query Match          30.7%; Score 120.6; DB 9; Length 532;
Best Local Similarity 93.3%; Pred. No. 8.4e-27;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATTTGAAAGCGTAACCACTGACGACACAAATGAAAGAAAGAAAGATTAAGTCGGTGAT 152
Db 231 GAATCTTGAAGACGTAACCACTGACGACACAAATGAAAGAAAGATTAAGTCGGTGAT 290
QY 153 TGTGAAAGAGACATTAAGAGACACATGTAAGGTGGAATAATGTAAGGCGCGAAAGTAACCTT 212
Db 291 TGTGAAAGAGACATTAAGAGACACATGTAAGGTGGAATAATGTAAGGCGCGAAAGTAACCTT 350
QY 213 ATGCATTTGTAATTT 227
Db 351 ATCACAAAGGAATCT 365

RESULT 15
US-09-847-057-4/c
; Sequence 4, Application US/09847057
; Patent No. US20020004943A1
GENERAL INFORMATION:
APPLICANT: AGRINOMICS, LLC.
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN F
FILE REFERENCE: PAGODA
CURRENT APPLICATION NUMBER: US/09/847,057
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 4

```

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 8340
; TYPE: DNA
; ORGANISM: Binary vector pAG14002
US-09-847-057-4

```

Query Match	30.7%	Score 120.6;	DB 10;	Length 8340;
Best Local Similarity	93.3%	Pred. NO. 3.1e-26;		
Matches 126; Conservative	0;	Mismatches 9;	Indels 0;	Gaps 0;

Qy	93	GAATATTGAAGACGTAGACGCTGACGACCAACAATGAAAGAGAAATTAAGTCCGTAT	152
Db	7853	GAACTTTGAAGACGTAGACGCTGACGACCAACAATGAAAGAGAAATTAAGTCCGTAT	7794
Qy	153	TGTGAAGAGACATAGACGACACATGTAAAGTGGAATAATGTAAGGCGGAAAGTAACCT	212
Db	7793	TGTGAAGAGACATAGACGACACATGTAAAGTGGAATAATGTAAGGCGGAAAGTAACCT	7734
Qy	213	ATGCATTTGTAATTT	227
Db	7733	ATGCACCAAGCAATCT	7719

Search completed: April 14, 2003, 12:29:05
Job time : 50.268 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:13:29 ; Search time 1585.51 Seconds

(without alignments)
6232.082 Million cell updates/sec

Title: US-09-963-803-19

Perfect score: 393

Sequence: 1 aagcttgatgcctgcagca.....cacacaacctagagatcc 393

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues 49582208

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /cgn2_6/ptodata/1/pna/US096B.COMB.seq:*
25: /cgn2_6/ptodata/1/pna/US096C.COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US096D.COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US096E.COMB.seq:*
28: /cgn2_6/ptodata/1/pna/US097A.COMB.seq:*
29: /cgn2_6/ptodata/1/pna/US097B.COMB.seq:*
30: /cgn2_6/ptodata/1/pna/US097C.COMB.seq:*
31: /cgn2_6/ptodata/1/pna/US098A.COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US098B.COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US098C.COMB.seq:*
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36: /cgn2_6/ptodata/1/pna/US099C.COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US099D.COMB.seq:*
38: /cgn2_6/ptodata/1/pna/US100A.COMB.seq:*
39: /cgn2_6/ptodata/1/pna/US100B.COMB.seq:*
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41: /cgn2_6/ptodata/1/pna/US101B.COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US102A.COMB.seq:*
43: /cgn2_6/ptodata/1/pna/US102B.COMB.seq:*

Result No.	Score	Query Match	Length	ID	Description
1	393	100.0	393	US-09-963-803-19	Sequence 19, Appl
2	314	79.9	462	US-09-963-803-20	Sequence 20, Appl
3	310	78.9	392	US-09-963-803-21	Sequence 21, Appl
4	304.6	77.5	600	US-09-963-803-22	Sequence 22, Appl
5	285.2	72.6	472	US-09-963-803-25	Sequence 25, Appl
6	214.4	54.6	317	US-09-963-803-3	Sequence 3, Appl
7	212.4	54.0	541	US-09-963-803-24	Sequence 24, Appl
8	200.4	51.0	348	US-09-963-803-23	Sequence 23, Appl
9	196.2	49.9	604	US-09-963-803-5	Sequence 5, Appl
10	154.8	39.4	371	US-09-963-803-6	Sequence 6, Appl
11	140.8	35.8	301	US-09-963-803-7	Sequence 7, Appl
12	140.8	35.8	398	US-09-963-803-8	Sequence 8, Appl
13	120.6	30.7	392	US-09-963-803-1	Sequence 1, Appl
14	120.6	30.7	392	US-09-963-803-1	Sequence 1, Appl
15	120.6	30.7	392	US-09-963-803-1	Sequence 1, Appl
16	120.6	30.7	392	US-09-963-803-1	Sequence 1, Appl
17	120.6	30.7	411	US-09-963-803-4	Sequence 4, Appl
18	120.6	30.7	411	US-09-963-803-4	Sequence 4, Appl
19	120.6	30.7	411	US-09-963-803-4	Sequence 4, Appl
20	120.6	30.7	411	US-09-963-803-4	Sequence 4, Appl
21	120.6	30.7	515	US-09-963-803-4	Sequence 4, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22 120.6 30.7 515 36 US-09-963-803-2 Sequence 2, Appl1
23 120.6 30.7 524 1 PCT-US97-10376-2 Sequence 2, Appl1
24 120.6 30.7 524 1 PCT-US97-10376A-2 Sequence 2, Appl1
25 120.6 30.7 524 16 US-09-202-838-2 Sequence 2, Appl1
26 120.6 30.7 524 16 US-09-202-838-3 Sequence 3, Appl1
27 120.6 30.7 524 16 US-09-202-838A-2 Sequence 2, Appl1
28 120.6 30.7 524 16 US-09-202-838A-3 Sequence 3, Appl1
29 120.6 30.7 526 1 PCT-US97-10376-3 Sequence 3, Appl1
30 120.6 30.7 532 30 US-09-765-555-1 Sequence 1, Appl1
31 120.6 30.7 532 30 US-09-673-274A-19 Sequence 19, Appl1
32 120.6 30.7 853 25 US-09-641-466-2 Sequence 2, Appl1
33 120.6 30.7 1036 26 US-09-673-274A-20 Sequence 20, Appl1
34 120.6 30.7 8340 32 US-09-847-057-4 Sequence 4, Appl1
35 120.6 30.7 8340 33 US-09-874-926-4 Sequence 5, Appl1
36 120.6 30.7 12241 1 PCT-US01-50638-5 Sequence 5, Appl1
37 120.6 30.7 12241 35 US-09-948-138-4 Sequence 5, Appl1
38 120.6 30.7 12241 38 US-10-033-190-5 Sequence 5, Appl1
39 120.6 30.7 305 1 PCT-US97-10376-5 Sequence 5, Appl1
40 117.4 29.9 305 1 PCT-US97-10376A-5 Sequence 5, Appl1
41 117.4 29.9 305 16 US-09-202-838A-5 Sequence 5, Appl1
42 117.4 29.9 305 16 US-09-202-838A-5 Sequence 5, Appl1
43 117.4 29.9 420 1 PCT-US97-10376-9 Sequence 9, Appl1
44 117.4 29.9 420 1 PCT-US97-10376A-9 Sequence 9, Appl1
45 117.4 29.9 420 1 PCT-US97-10376A-9 Sequence 9, Appl1
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ALIGNMENTS

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RESULT 1
US-09-963-803-19
: Sequence 19, Application US/09963803
: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
: FILE REFERENCE: 184332042
: CURRENT APPLICATION NUMBER: US/09/963, 803
: PRIOR FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: FR 99/03925
: PRIOR FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: PCT IB00/00370
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 19
: LENGTH: 393
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: promoter Mp1162
: NAME/KEY: promoter
: LOCATION: (1)..(393)
: OTHER INFORMATION:
US-09-963-803-19
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Query Match 100.0%; Score 393; DB 36; Length 393;

Best Local Similarity 100.0%; Pred. No. 2, 6e-103; Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 AAGCTTGATGCGCTGCAGACAGTATGCGCGGTGATCATCAATGACATCATCAGAGTACTGA 60
Db 1 AAGCTTGATGCGCTGCAGACAGTATGCGCGGTGATCATCAATGACATCATCAGAGTACTGA 60
Oy 61 GGAGATGATAGTACCTGACACTCTGTGCGAATATTGAAGAGCTAGACACTGACGAC 120
Db 61 GGAGATGATAGTACCTGACACTCTGTGCGAATATTGAAGAGCTAGACACTGACGAC 120
Oy 121 AACCATGAAAAGACAGTAAGTACGCGATTTGGAAGAGACATAGAGGACACATGTA 180
Db 121 AACCATGAAAAGACAGTAAGTACGCGATTTGGAAGAGACATAGAGGACACATGTA 180
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Oy 181 AGGTGAAAATGTAGAGCGGGAAGTAACTTATGATTTGTTAAATTGGTTACGACTAGT 240
Db 181 AGGTGAAAATGTAGAGCGGGAAGTAACTTATGATTTGTTAAATTGGTTACGACTAGT 240
Oy 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGATGACCATGCC 300
Db 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGATGACCATGCC 300
Oy 301 ACGTAAACCGGATGCCGCTGCCAAGCTTATTTCTTATTTAAGCACTGTGTAGTAG 360
Db 301 ACGTAAACCGGATGCCGCTGCCAAGCTTATTTCTTATTTAAGCACTGTGTAGTAG 360
Oy 361 CTTAGAAAACCAACACACACTAGAGATCC 393
Db 361 CTTAGAAAACCAACACACACTAGAGATCC 393
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RESULT 2
US-09-963-803-20
: Sequence 20, Application US/09963803
: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
: FILE REFERENCE: 184332042
: CURRENT APPLICATION NUMBER: US/09/963, 803
: PRIOR FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: FR 99/03925
: PRIOR FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: PCT IB00/00370
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 20
: LENGTH: 462
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: promoter Mp1163
: NAME/KEY: promoter
: LOCATION: (1)..(462)
: OTHER INFORMATION:
US-09-963-803-20
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Query Match 79.9%; Score 314; DB 36; Length 462;

Best Local Similarity 85.1%; Pred. No. 2, 5e-80; Matches 393; Conservative 0; Mismatches 0; Indels 69; Gaps 1;

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Oy 1 AAGCTTGATGCGCTGCAGACAGTATGCGCGGTGATCATCAATGACATCATCAGTACTGA 60
Db 1 AAGCTTGATGCGCTGCAGACAGTATGCGCGGTGATCATCAATGACATCATCAGTACTGA 60
Oy 61 GGAGATGATAGTACCTGACACTCTGTGCGAATATTGAAGAGCTAGACACTGACGAC 120
Db 61 GGAGATGATAGTACCTGACACTCTGTGCGAATATTGAAGAGCTAGACACTGACGAC 120
Oy 121 AACCATGAAAAGACAGTAAGTACGCGATTTGGAAGAGACATAGAGGACACATGTA 180
Db 121 AACCATGAAAAGACAGTAAGTACGCGATTTGGAAGAGACATAGAGGACACATGTA 180
Oy 181 AGGTGAAAATGTAGAGCGGGAAGTAACTTATGATTTGTTAAATTGGTT----- 231
Db 181 AGGTGAAAATGTAGAGCGGGAAGTAACTTATGATTTGTTAAATTGGTTAGCACTAGT 240
Oy 232 ----- 231
Db 241 GATTGATGTATATCAAGATTGATGTGATATCTCCACTGACGTAAGGATGACGATGCC 300
Oy 232 ACGACTAGATGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGATG 291
Db 301 ACGACTAGATGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGATG 360
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MP11169
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(472)
OTHER INFORMATION:
US-09-963-803-25

Query Match 72.6%; Score 285.2; DB 36; Length 472;
Best Local Similarity 98.1%; Pred. No. 5.8e-72;
Matches 310; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

QY 78 CATGACACTCTGCGCAATATTGAAGACGTAAGCAGTACGACGACACAAATGAAGAAGAA 137
DB 160 CATGCCACTCTGCGCAATATTGAAGACGTAAGCAGTACGACGACACAAATGAAGAAGAA 219
QY 138 GATAGCGTGGTATTTGTGAAGACATAGAGACATGTAAGGTGAAAAATGTAAGG 197
DB 220 GATAGCGTGGTATTTGTG-AAGACATAGAGACATGTAAGGTGAAAAATGTAAGG 278
QY 198 GCGGAAGTAACCTTATGCTTGTATTTGTAGTACGACATGATGATGATATCAA 257
DB 279 GCGGAAGTAACCTTATGCTTGTATTTGTAGTACGACATGATGATGATATCAA 338
QY 258 GATTGATGTATATCTCCACTGACGTAAGGATGACGATGCCGTTACCGGTATGCC 317
DB 339 GATTGATGTATATCTCCACTGACGTAAGGATGACGATGCCGTTACCGGTATGCC 398
QY 318 GGTTCACACCTTTATTTCTTTATTAAGCAGTGTGTAGTACCTTAAGAAACCAACACA 377
DB 399 GGTTCACACCTTTATTTCTTTATTAAGCAGTGTGTAGTACCTTAAGAAACCAACACA 456
QY 378 ACAACCTAGAGATCC 393
DB 457 ACAACCTAGAGATCC 472

RESULT 6

US-09-963-803-3
Sequence 3, Application US/09963803
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 317
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter MP1116
NAME/KEY: promoter
LOCATION: (1)..(317)
OTHER INFORMATION:
US-09-963-803-3

Query Match 54.6%; Score 214.4; DB 36; Length 317;
Best Local Similarity 79.9%; Pred. No. 1.9e-51;
Matches 299; Conservative 0; Mismatches 1; Indels 74; Gaps 1;

QY 20 ACTAGATATCCCGCGTATCATATATCATCATCATAGTACTAGAGATGAATACTAGCCA 79
DB 18 ACTAGATATCCCGCGTATCATATATCATCATCATAGTACTAGAGATGAATACTAGCCA 77

QY 80 TGACACTCTGTGCGAATATTGAAGACGTAAGCAGTACGACGACAAATGAAGAAGAGA 139
DB 78 TGACACTCTGTGCGAATATTGAAGACGTAAGCAGTACGACGACAAATGAAGAAGAGA 137
QY 140 TAAGTCGGTGAATTTGAAAGACATAGACGACATGTAAGGTGGAATAATGTAAGGCC 199
DB 138 TAAGTCGGTGAATTTGAAAGACATAGACGACATGTAAGGTGGAATAATGTAAGGCC 197
QY 200 GGAATTAACCTTATTCATTTTGTATTTGTTAGTACGACTAGTATGATGATATCAAGA 259
DB 198 GGAATTAACCTTATTCATTTTGTATTTGTTAGTACGACTAGTATGATGATATCAAGA 226
QY 260 TTGATGTGATATCTCCAGTACGATAGGATGACGATGCCAGTTACCGGATGCGG 319
DB 227 -----GTTACCGGATGCGG 243
QY 320 TTCCCAAGCTTTATTTCTTATTTTAAGCACTTGTGTAGTATGTAAGAAACCAACACAC 379
DB 244 TTCCCAAGCTTTATTTCTTATTTTAAGCACTTGTGTAGTATGTAAGAAACCAACACAC 303
QY 380 AACCTAGAGATCC 393
DB 304 AACCTAGAGATCC 317

RESULT 7

US-09-963-803-24
Sequence 24, Application US/09963803
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 541
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MP11168
NAME/KEY: promoter
LOCATION: (1)..(541)
OTHER INFORMATION:
US-09-963-803-24

Query Match 54.0%; Score 212.4; DB 36; Length 541;
Best Local Similarity 91.5%; Pred. No. 8.7e-51;
Matches 236; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 78 CATGACACTCTGCGCAATATTGAAGACGTAAGCAGTACGACGACAAATGAAGAAGAA 137
DB 160 CATGCCACTCTGCGCAATATTGAAGACGTAAGCAGTACGACGACAAATGAAGAAGAA 219
QY 138 GATAGCGTGGTATTTGTGAAGACATAGAGACATGTAAGGTGGAATAATGTAAGG 197
DB 220 GATAGCGTGGTATTTGTG-AAGACATAGAGACATGTAAGGTGGAATAATGTAAGG 278
QY 198 GCGGAAGTAACCTTATGCTTGTATTTGTAGTACGACATGATGATGATATCAA 257
DB 279 GCGGAAGTAACCTTATGCTTGTATTTGTAGTACGACATGATGATGATATCAA 338
QY 258 GATTGATGTATATCTCCACTGACGTAAGGATGACGATGCCGTTACCGGTATGCC 317
DB 339 GATTGATGTATATCTCCACTGACGTAAGGATGACGATGCCGTTACCGGTATGCC 398


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Db 250 GCGGAAAGTAACCTTATGCACTTTGTAACCTG----- 280
QY 258 GATTGATGTGATATCTCCACTGACGTAAGGATGACGATGCACGTTACCGGTATGCC 317
    |||||||
Db 281 -----GTTACCGCGGTATGCC 295
QY 318 GGTTCACCACTTATTTCTTATTTAAGACACTGTGTAGTACTTAGAAGAACCAACACA 377
    |||||||
Db 296 GGTTCACCACTTATTTCTTATTTAAGACACTGTGTAGTACTTAGAAGAACCAACACA 355
QY 378 ACAACCTAGAGATCC 393
Db 356 ACAACCTAGAGATCC 371

RESULT 11
US-09-963-803-7
; Sequence 7, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963, 803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter Mpr1154
; NAME/KEY: promoter
; LOCATION: (1)..(301)
; OTHER INFORMATION:
US-09-963-803-7

Query Match          35.8%; Score 140.8; DB 36; Length 301;
Best Local Similarity 98.1%; Pred. No. 4.5e-30;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 78 CATGACACTGTGCGCAATTTTGAAGACGTAGACACTGACGACACATGAAAAAGAGAA 137
    |||||||
Db 63 CATGCCACTCTGTGCGAATTTTGAAGACGTAGACACTGACGACACATGAAAAAGAGAA 122
QY 138 GATAAGTGGTATTTGTGAAGACATGAGACATGTAAGGTGAAAAATGTAAGG 197
    |||||||
Db 123 GATAAGTGGTATTTGTGAAGACATGAGACATGTAAGGTGAAAAATGTAAGG 181
QY 198 GCGGAAAGTAACCTTATGCACTTTGTAATTTGTTAC 233
    |||||||
Db 182 GCGGAAAGTAACCTTATGCACTTTGTAATTTGTTAC 217

RESULT 12
US-09-963-803-6
; Sequence 6, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963, 803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
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; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter Mpr1147
; NAME/KEY: promoter
; LOCATION: (1)..(398)
; OTHER INFORMATION:
US-09-963-803-6

Query Match          35.8%; Score 140.8; DB 36; Length 398;
Best Local Similarity 98.1%; Pred. No. 5e-30;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 78 CATGACACTGTGCGCAATTTTGAAGACGTAGACACTGACGACACATGAAAAAGAGAA 137
    |||||||
Db 160 CATGCCACTCTGTGCGAATTTTGAAGACGTAGACACTGACGACACATGAAAAAGAGAA 219
QY 138 GATAAGTGGTATTTGTGAAGACATGAGACATGTAAGGTGAAAAATGTAAGG 197
    |||||||
Db 220 GATAAGTGGTATTTGTGAAGACATGAGACATGTAAGGTGAAAAATGTAAGG 278
QY 198 GCGGAAAGTAACCTTATGCACTTTGTAATTTGTTAC 233
    |||||||
Db 279 GCGGAAAGTAACCTTATGCACTTTGTAATTTGTTAC 314

RESULT 13
PCT-US97-10376-1
; Sequence 1, Application PC/TUS9710376
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CASSAVA VEIN MOSAIC VIRUS PROMOTERS AND
; FILE REFERENCE: US97/10376
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/10376
; FILING DATE: 20-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,129
; FILING DATE: 20-JUN-1996
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; HYPOTHETICAL: NO
; PCT-US97-10376-1

Query Match          30.7%; Score 120.6; DB 1; Length 392;
Best Local Similarity 93.3%; Pred. No. 3.7e-24;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGACGTAGACACTGACGACACATGTAAGAAAGAAAGATAGGTGGTGAT 152
    |||||||
Db 143 GATCTTGAAGACGTAGACACTGACGACACATGTAAGAAAGAAAGATAGGTGGTGAT 202
QY 153 TGTGAAGACATGAGACACATGTAAGGTGGAAGTGAAGGGCGGAAGTAACCTT 212
    |||||||
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Db 203 TGTGAAGAGACATAGAGACACATGTAAAGTGGAAAATGTAAGCGCGGAAGTAACCTT 262

QY 213 ATGCATTGTAAATT 227

Db 263 ATCACAAGGAATCT 277

RESULT 14

PCT-US97-10376A-1
; Sequence 1, Application PC/TUS9710376A
; GENERAL INFORMATION:
; APPLICANT: Verdaguier, Bertrand
; APPLICANT: de Kochko, Alexandre
; APPLICANT: Beachy, Roger N.
; TITLE OF INVENTION: CASSAVA VEIN MOSAIC VIRUS PROMOTERS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10550 North Torrey Pines Road
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/10376A
; FILING DATE: 20-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,129
; FILING DATE: 20-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: 504.1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
PCT-US97-10376A-1

Query Match 30.7%; Score 120.6; DB 1; Length 392;

Best Local Similarity 93.3%; Pred. No. 3.7e-24;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGACGTAGACACTGACGACAAACATGAAAGAGAAAGTAAGTGGTGAT 152

Db 143 GAATCTTGAAGACGTAGACACTGACGACAAACATGAAAGAGAAAGTAAGTGGTGAT 202

QY 153 TGTGAAGAGACATAGAGACACATGTAAAGTGGAAAATGTAAGCGCGGAAGTAACCTT 212

Db 203 TGTGAAGAGACATAGAGACACATGTAAAGTGGAAAATGTAAGCGCGGAAGTAACCTT 262

QY 213 ATGCATTGTAAATT 227

Db 263 ATCACAAGGAATCT 277

RESULT 15

US-09-202-838-1

; Sequence 1, Application US/09202838
; GENERAL INFORMATION:
; APPLICANT: Verdaguier, Bertrand
; APPLICANT: de Kochko, Alexandre
; APPLICANT: Beachy, Roger N.
; APPLICANT: Fauquet, Claude
; TITLE OF INVENTION: CASSAVA VEIN MOSAIC VIRUS PROMOTERS AND USES THEREOF
; FILE REFERENCE: MYC0115
; CURRENT APPLICATION NUMBER: US/09/202,838
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/US97/10376
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: 60/020,129
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Cassava vein mosaic virus
US-09-202-838-1

Query Match 30.7%; Score 120.6; DB 16; Length 392;

Best Local Similarity 93.3%; Pred. No. 3.7e-24;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGACGTAGACACTGACGACAAACATGAAAGAGAAAGTAAGTGGTGAT 152

Db 143 GAATCTTGAAGACGTAGACACTGACGACAAACATGAAAGAGAAAGTAAGTGGTGAT 202

QY 153 TGTGAAGAGACATAGAGACACATGTAAAGTGGAAAATGTAAGCGCGGAAGTAACCTT 212

Db 203 TGTGAAGAGACATAGAGACACATGTAAAGTGGAAAATGTAAGCGCGGAAGTAACCTT 262

QY 213 ATGCATTGTAAATT 227

Db 263 ATCACAAGGAATCT 277

Search completed: April 14, 2003, 12:06:29
Job time : 1588.51 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:19:51 : Search time 311.159 Seconds
(without alignments)
5404.014 Million cell updates/sec

Title: US-09-963-803-19

Perfect score: 393

Sequence: 1 aagcttcagctgcgcagca.....cacaacacactagagatcc 393

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 5824060 seqs, 2139321184 residues

Total number of hits satisfying chosen parameters: 11648120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
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11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120.6	30.7	532	6	US-09-765-555A-1
2	120.6	30.7	838	6	US-09-673-274B-19
3	120.6	30.7	1036	6	US-09-673-274B-20
4	39.8	10.1	250715	7	US-09-949-016-13294
5	39	9.9	309	8	US-10-380-935-30
6	39	9.9	522	8	US-10-380-935-37
7	39	9.9	835	8	US-10-391-414-10
8	39	9.9	1683	11	US-60-434-166-147
9	39	9.9	3261	9	US-10-302-267-1
10	39	9.9	3212	9	US-10-130-150-13
11	39	9.9	3288	9	US-10-130-150-18
12	39	9.9	3329	9	US-10-130-150-15
13	39	9.9	5247	9	US-10-160-764-40
14	39	9.9	5250	9	US-10-160-764-4
15	39	9.9	5511	9	US-10-160-764-48
16	39	9.9	5715	9	US-10-160-764-52
17	39	9.9	5796	8	US-10-378-810-2
18	39	9.9	6285	9	US-10-160-764-42
19	39	9.9	6299	9	US-10-160-764-50
20	39	9.9	8349	9	US-10-198-478-16
21	39	9.9	10249	9	US-10-198-478-14
22	39	9.9	10312	9	US-10-198-478-15

23	39	9.9	10339	9	US-10-198-478-13	Sequence 13, Appl
24	39	9.9	13737	6	US-09-538-414-10	Sequence 10, Appl
25	37.4	9.5	206	9	US-10-204-889-9	Sequence 9, Appl
26	37.4	9.5	382	1	PCT-US02-17853-22	Sequence 22, Appl
27	37.4	9.5	842	9	US-10-321-434-6	Sequence 6, Appl
28	37.4	9.5	2267	1	PCT-US02-17853-11	Sequence 11, Appl
29	37.4	9.5	2873	1	PCT-US03-03435-55	Sequence 55, Appl
30	37.4	9.5	2873	9	US-10-353-454-38	Sequence 38, Appl
31	37.4	9.5	2873	9	US-10-356-088-55	Sequence 55, Appl
32	37.4	9.5	3002	9	US-10-353-454-37	Sequence 48, Appl
33	37.4	9.5	3034	1	PCT-US03-03435-48	Sequence 48, Appl
34	37.4	9.5	3034	9	US-10-353-454-31	Sequence 31, Appl
35	37.4	9.5	3034	9	US-10-356-088-48	Sequence 48, Appl
36	37.4	9.5	4182	5	US-09-921-922A-7	Sequence 7, Appl
37	37.4	9.5	5449	1	PCT-US03-03435-57	Sequence 57, Appl
38	37.4	9.5	5449	9	US-10-353-454-40	Sequence 40, Appl
39	37.4	9.5	5449	9	US-10-356-088-57	Sequence 57, Appl
40	37.4	9.5	6975	6	US-09-464-528C-17	Sequence 17, Appl
41	37.4	9.5	9555	5	US-09-921-922A-6	Sequence 6, Appl
42	37.4	9.5	13199	9	US-10-137-325A-2	Sequence 2, Appl
43	37.4	9.5	17476	8	US-10-385-546-7	Sequence 7, Appl
44	37	9.4	5195	9	US-10-311-455-893	Sequence 893, App
45	37	9.4	6944	9	US-10-311-506-113	Sequence 113, App

ALIGNMENTS

RESULT 1
US-09-765-555A-1
: Sequence 1, Application US/0976555A
: GENERAL INFORMATION:
: APPLICANT: The Scripps Research Institute
: APPLICANT: Barbas, Carlos
: APPLICANT: Stege, Justin
: APPLICANT: Guan, Xueni
: APPLICANT: Delmia, Bipin
: TITLE OR INVENTION: Methods and compositions to modulate
: FILE REFERENCE: 27801-20014.20
: CURRENT APPLICATION NUMBER: US/09/765,555A
: PRIOR FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: 09/620,897
: PRIOR FILING DATE: 2000-07-21
: PRIOR APPLICATION NUMBER: US 60/177,468
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 532
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Promoter C&MV
US-09-765-555A-1
Query Match 30.7%; Score 120.6; DB 6; Length 532;
Best Local Similarity 93.3%; Pred. No. 1.2e-25;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY	93	GAATTTGAAGACCTAGCATGACGACACAAAGAAAGAAAGTAAGTGGTGGAT	152
DB	231	GAATCTTGAAGACCTAGCATGACGACACAAAGAAAGAAAGTAAGTGGTGGAT	290
QY	153	TGTGAAGAGACATAGAGACACATGTAAGGTGGAATATGTAAGCGCGAAAGTAACCT	212
DB	291	TGTGAAGAGACATAGAGACACATGTAAGGTGGAATATGTAAGCGCGAAAGTAACCT	350
QY	213	ATGCATTTGTAATTT	227
DB	351	ATCACAAGGAATCT	365

```

RESULT 2
US-09-673-274B-19
: Sequence 19, Application US/09673274B
: GENERAL INFORMATION:
:   APPLICANT: Lamberty, Mireille
:   APPLICANT: Bulet, Philippe
:   APPLICANT: Brookhart, Gary
:   APPLICANT: Hoffmann, Jules
:   TITLE OF INVENTION: GENE CODING FOR HELIOMICINE, AND USE THEREOF
:   FILE REFERENCE: A33595-PCT-USA (0726667.0166)
:   CURRENT APPLICATION NUMBER: US/09/673,274B
:   PRIOR FILING DATE: 1999-04-12
:   PRIOR APPLICATION NUMBER: PCT/FR99/00843
:   PRIOR FILING DATE: 1999-04-12
:   PRIOR APPLICATION NUMBER: FR 98 04933
:   NUMBER OF SEQ ID NOS: 48
:   SOFTWARE: FastSeq for Windows Version 4.0
:   SEQ ID NO 19
:   LENGTH: 838
:   TYPE: DNA
:   ORGANISM: Artificial Sequence
:   FEATURE:
:   OTHER INFORMATION: Synthetic oligonucleotide
:   FEATURE:
:   NAME/KEY: promoter
:   LOCATION: (7)...(532)
:   FEATURE:
:   NAME/KEY: misc_structure
:   LOCATION: (533)...(568)
:   FEATURE:
:   NAME/KEY: terminator
:   LOCATION: (569)...(832)
:   US-09-673-274B-19

Query Match          30.7%: Score 120.6; DB 6; Length 838;
Best Local Similarity 93.3%: Pred. No. 1.4e-25;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      93  GAATATTGGAAGACGCTAAGCAGTACGACGACACAAATGTAAGGCGGTAACCTT 152
Db      222  GAATCTTGAAAGACGTAACGACCTGACGACACAAATGTAAGGCGGTAACCTT 281

QY      153  TGTGAAGAGACATAGAGACACATGTAAAGTGGAAATGTAAAGCGCGGAAGTAACCTT 212
Db      282  TGTGAAGAGACATAGAGACACATGTAAAGTGGAAATGTAAAGCGCGGAAGTAACCTT 341

QY      213  ATGCATTGTAACTT 227
Db      342  ATCACAAGGAATCT 356

RESULT 3
US-09-673-274B-20
: Sequence 20, Application US/09673274B
: GENERAL INFORMATION:
:   APPLICANT: Lamberty, Mireille
:   APPLICANT: Bulet, Philippe
:   APPLICANT: Brookhart, Gary
:   APPLICANT: Hoffmann, Jules
:   TITLE OF INVENTION: GENE CODING FOR HELIOMICINE, AND USE THEREOF
:   FILE REFERENCE: A33595-PCT-USA (0726667.0166)
:   CURRENT APPLICATION NUMBER: US/09/673,274B
:   PRIOR FILING DATE: 1999-04-12
:   PRIOR APPLICATION NUMBER: PCT/FR99/00843
:   PRIOR FILING DATE: 1999-04-12
:   PRIOR APPLICATION NUMBER: FR 98 04933
:   NUMBER OF SEQ ID NOS: 48
:   SOFTWARE: FastSeq for Windows Version 4.0
:   SEQ ID NO 20
:   LENGTH: 1036
:   TYPE: DNA

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? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Synthetic oligonucleotide
? FEATURE:
? NAME/KEY: promoter
? LOCATION: (7)...(532)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (539)...(736)
? FEATURE:
? NAME/KEY: terminator
? LOCATION: (767)...(1030)
US-09-673-274B-20

Query Match          30.7%   Score 120.6;   DB: 6;   Length 1036;
Best Local Similarity 93.3%   Pred. No. 1.5e-25;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      93  GAATTTTGAAGACGTAAACACTGACGACACAAATATAAAGAAGATTAAGTGGTGAT 152
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      222  GAATCTTTAAGACGCTAAACACTGACGACACAAATATAAAGAAGATTAAGTCCGTAT 281

QY      153  TGTGAAGAAGACATTAAGAGACACATGTAAAGTGTGAAAAATGTAAAGGCGGAAAGTAACCTT 212
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      282  TGTGAAGAAGACATTAAGAGACACATGTAAAGTGTGAAAAATGTAAAGGCGGAAAGTAACCTT 341

QY      213  ATGCATTTGTAAATT 227
      || | || | || |
Db      342  ATCACAAAGGAATCT 356

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RESULT 4
US-09-949-016-13294
Sequence 13294, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY FILING DATE: 2000-04-14
PRIORITY FILING DATE: 2000-10-20
PRIORITY FILING DATE: 2000-10-20
PRIORITY FILING DATE: 2000-10-03
PRIORITY FILING DATE: 2000-09-08
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ. ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13294
LENGTH: 250715
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(250715)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13294

Query Match          10.1%; Score 39.8; DB 7; Length 250715;
Best Local Similarity 52.0%; Pred. No. 0.62;
Matches 89; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

OY      119  ACAACATGAAAGACAGATAGGTCGGTGATTTGTGAAGACACATAGAGACACATG 178
          | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 146653 AGAAGAAAGGAGAAAGAAAGAAAGAAAGAAAGGAGAGAAAGGAGAAAGAAAG 146712

OY      179  TAAGGTGAAATAGTAAGGCGGAAGTAACTTATGCATTTGTATTGTTAGACTA 238
          | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 146713 AAAAGAAAGAAACCTCTACTATGAAATTAATAATTAATTCAGTTATTTTACTTGATTA 146772

OY      239  GTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAGAGGA 289
          | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 146773 ATGTGTGATGCGTGATACACAGATAAATAAATAAATAAAGA 146823

RESULT 5

US-10-380-935-30
; Sequence 30, Application US/10380935
; GENERAL INFORMATION:
; APPLICANT: WARNER, Simon, Anthony, James
; APPLICANT: HARKES, Timothy, Robert
; APPLICANT: ANDREWS, Christopher, John
; TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: PPD50594/MO
; CURRENT APPLICATION NUMBER: US/10/380,935
; PRIOR FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: GB0023911.1
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: GB0027693.1
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: GB0023910.3
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 309
; TYPE: DNA
; ORGANISM: Cauliflower Mosaic Virus
; FEATURE:
; OTHER INFORMATION: Enhancer
US-10-380-935-30

Query Match

Best Local Similarity 9.9%; Score 39; DB 8; Length 309;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
Db 242 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 280

RESULT 6

US-10-380-935-37
; Sequence 37, Application US/10380935
; GENERAL INFORMATION:
; APPLICANT: WARNER, Simon, Anthony, James
; APPLICANT: HARKES, Timothy, Robert
; APPLICANT: ANDREWS, Christopher, John
; TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: PPD50594/MO
; CURRENT APPLICATION NUMBER: US/10/380,935
; PRIOR FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: GB0023911.1
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: GB0027693.1
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: GB0023910.3
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Figwort Mosaic Virus
; FEATURE:
; OTHER INFORMATION: Enhancer
US-10-380-935-37

Query Match

Best Local Similarity 9.9%; Score 39; DB 8; Length 522;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
Db 459 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 497

RESULT 7

US-10-391-414-10
; Sequence 10, Application US/10391414
; GENERAL INFORMATION:
; APPLICANT: SHINOZAKI, Kazuko
; APPLICANT: KATSURA, Koji
; APPLICANT: ITO, Yusuke
; TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
; FILE REFERENCE: 382.1041
; CURRENT APPLICATION NUMBER: US/10/391,414
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: JP 2002-377316
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 835
; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-10-391-414-10

Query Match

Best Local Similarity 9.9%; Score 39; DB 8; Length 835;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
Db 729 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 767

RESULT 8

US-60-434-166-147
; Sequence 147, Application US/60434166
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology
; APPLICANT: Creelman, Robert A.
; APPLICANT: Haake, Volker
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Adam, Luc J.
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0051 P
; CURRENT APPLICATION NUMBER: US/60/434,166
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 559
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G2227
US-60-434-166-147

Query Match

Best Local Similarity 9.9%; Score 39; DB 11; Length 1683;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
Db 9 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 47

RESULT 9

US-10-302-267-1
; Sequence 1, Application US/10302267
; GENERAL INFORMATION:

```
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein
US-10-130-150-13
Query Match          9.9%; Score 39; DB 9; Length 2361;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAGGATGACGCA 296
DB 113 GATTGATGTGATATCTCCACTGACGTAGGATGACGCA 151

RESULT 10
US-10-130-150-13
; Sequence 13, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
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```
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein
US-10-130-150-13
Query Match          9.9%; Score 39; DB 9; Length 3212;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAGGATGACGCA 296
DB 197 GATTGATGTGATATCTCCACTGACGTAGGATGACGCA 235

RESULT 11
US-10-130-150-18
; Sequence 18, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein fuse
US-10-130-150-18
Query Match          9.9%; Score 39; DB 9; Length 3288;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAGGATGACGCA 296
DB 197 GATTGATGTGATATCTCCACTGACGTAGGATGACGCA 235

RESULT 12
US-10-130-150-15
; Sequence 15, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 3329
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein fuse
US-10-130-150-15
Query Match          9.9%; Score 39; DB 9; Length 3329;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAGGATGACGCA 296
DB 197 GATTGATGTGATATCTCCACTGACGTAGGATGACGCA 235

RESULT 13
US-10-160-764-40
; Sequence 40, Application US/10160764
```

```

; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailfoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 5247
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; OTHER INFORMATION: pBI121-35S-AtFTa
US-10-160-764-40

Query Match          9.9%; Score 39; DB 9; Length 5247;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
DB 3209 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 3247

RESULT 14
US-10-160-764-4
; Sequence 4, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailfoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5250
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; OTHER INFORMATION: pBI121-35S-anti-AtFTa sequence
US-10-160-764-4

Query Match          9.9%; Score 39; DB 9; Length 5250;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
DB 3209 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 3247
```

```

RESULT 15
US-10-160-764-48
; Sequence 48, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailfoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 5511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; OTHER INFORMATION: pBI121-35S-Anti-AtFTa
US-10-160-764-48

Query Match          9.9%; Score 39; DB 9; Length 5511;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
DB 3209 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 3247
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Title: US-09-963-803-19
Perfect score: 393
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1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42.4	10.8	224	17	BH746858 SALK_0036
2	42.4	10.8	561	13	BM162517 EST565040
3	41	10.4	222	13	BM161725 EST564248
4	40.2	10.2	528	9	AL369550 MCB31610
5	40	10.2	911	17	AZ548969 ENT2M27TF
6	39.2	10.0	480	17	BH639017 1008026H0

7	39	9.9	112	17	BH751161 SALK_0494
8	39	9.9	142	17	BH749349 SALK_0477
9	39	9.9	153	17	BH619283 SALK_0407
10	39	9.9	153	17	BH747013 SALK_0080
11	39	9.9	158	17	BH748291 SALK_0451
12	39	9.9	165	17	BH747357 SALK_0165
13	39	9.9	175	17	BH746616 SALK_0452
14	39	9.9	177	17	BH802465 1008026E1
15	39	9.9	190	17	BH752801 SALK_0193
16	39	9.9	193	17	BH748289 SALK_0450
17	39	9.9	214	17	BH747829 SALK_0353
18	39	9.9	215	17	BH753813 SALK_0296
19	39	9.9	219	17	BH747744 SALK_0337
20	39	9.9	220	17	BH747438 SALK_0174
21	39	9.9	221	17	BH802415 1008026B0
22	39	9.9	230	17	BH746474 SALK_0428
23	39	9.9	230	17	BH799173 1008025B1
24	39	9.9	237	17	BH802463 1008026E0
25	39	9.9	244	17	BH746375 SALK_0402
26	39	9.9	248	17	BH254798 SALK_0172
27	39	9.9	251	17	BH750121 SALK_0371
28	39	9.9	254	17	BH748500 SALK_0460
29	39	9.9	256	17	BH748499 SALK_0460
30	39	9.9	258	17	BH802470 1008026F0
31	39	9.9	261	17	BH802493 1008026H0
32	39	9.9	268	17	BH611919 SALK_0318
33	39	9.9	269	17	BH211646 SALK_0064
34	39	9.9	269	17	BH802489 1008026G0
35	39	9.9	271	17	BH799178 1008025C0
36	39	9.9	272	17	BH802428 1008026C0
37	39	9.9	274	17	BH802495 1008026H0
38	39	9.9	279	17	BH748475 SALK_0460
39	39	9.9	281	17	BH750170 SALK_0371
40	39	9.9	281	17	BH802443 1008026D0
41	39	9.9	284	17	BH213307 SALK_0090
42	39	9.9	284	17	BH746665 SALK_0457
43	39	9.9	286	17	BH747007 SALK_0078
44	39	9.9	293	17	BH610310 SALK_0085
45	39	9.9	296	17	BH213532 SALK_0093

ALIGNMENTS

RESULT 1
BH746858
LOCUS
DEFINITION
SALK_003694.51.40.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_003694.51.40.x, DNA
sequence.

ACCESSION
BH746858
VERSION
BH746858.1 GI:18959973

KEYWORDS
SOURCE
ORGANISM

thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab,
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.

TITLE
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker

JOURNAL
COMMENT
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of

/organism="Plasmodium yoelii yoelii"
 /strain="17XL"
 /db_xref="taxon:73239"
 /clone="PYCMT64"
 /clone_lib="PYBS"
 /dev_stage="Asexual blood stages"
 /lab_host="E. coli XL-1 Blue"
 /note="Vector: pMD-GAL4. At 20-25% parasitemia, blood was
 collected from BALB/cBy mice infected with Py17XL
 parasites, and leukocytes removed by passage over
 microcrystalline cellulose columns. Total RNA was
 isolated using the guanidinium isothiocyanate method,
 and RNA isolated using oligo(dT)-cellulose chromatography.
 First strand cDNA synthesis was completed using a 50-base
 primer and reverse transcriptase in the presence of
 5-methyl dCTP. After second strand synthesis, uneven
 termini were treated with Pfu DNA polymerase and EcoRI

/organism="Plasmodium yoelli yoelli"
 /strain="17XL"
 /db_xref="taxon:73239"
 /clone_11b="PYBS"
 /dev_stage="Asexual blood stages"
 /lab_host="E. coli XL-1 Blue"
 /note="Vector: pMD-GM4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, unexen 5-merm1 were treated with Pfu DNA polymerase and EcoRI

adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybridZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybridZAP vector and plasmid DNA isolated."

BASE COUNT 99 a 25 c 38 g 60 t
ORIGIN

Query Match 10.4%; Score 41; DB 13; Length 222;

Best Local Similarity 53.4%; Pred. No. 1.9;

Matches 86; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

OY 88 TGGCGCAATTTGAAGCGTACGACACGACACAAATGAAAAGAAAGATAGGTCG 147

DB 10 TGTAAAAAGATAGATATATATATACACACAGCTGCTGAAAATGCGAAATGCG 69

OY 148 GTGATTGTGAAGACATGAGACACATGTAAAGTGAAATGTAAAGCGCGAAAGTA 207

DB 70 GAATTTATGAAAATGGCTGACGAGTACATAAATGAAATGAAATCAATCGAAATGAA 129

OY 208 ACCTTATGCATTGTATTTGTTAGCAGCTAGCATGATGATG 248

DB 130 GGGCGAAGCAATCATATATATTTATGCTTATATTTATG 170

RESULT 4

AL369550

LOCUS

DEFINITION MTBA31G10R1 MTBA Medicago truncatula cDNA clone MTBA31G10 T7, mRNA

sequence.

ACCESSION

AL369550

VERSION AL369550.1 GI:9669303

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1.528
/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MTBA31G10"
/clone_lib="MTBA"
/tissue_type="root tips"
/dev_stage="harvested after 3 days of N-starvation"
/note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2: XhoI; Plants were grown in an aeroponic chamber for 14 days on nitrogen-rich medium followed by 3 days on N-free medium. RNA was extracted from root tips (1-3 cm). cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-ZapXX vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were

mass-excised from phage stocks using ExsacII helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France)."

BASE COUNT 173 a 50 c 136 g 169 t
ORIGIN

Query Match 10.2%; Score 40.2; DB 9; Length 528;

Best Local Similarity 47.1%; Pred. No. 3.5; 138; Indels 0; Gaps 0;

Matches 123; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

OY 129 AAGAGAGAGATTAAGTCGCTGATTTGAAAGACATAGACACATTAAGTGGA 188

DB 254 AAGACTTTCATAGATGTTCTCATGATAGAGATATATATCATTTGAAGCGTAAG 313

OY 189 AATGTAAAGCGCGAAAGTAACCTTATGATTTGTTAAATGTTAGCATGATGATG 248

DB 314 AATTTGATTTGATTTAATTAAGGCTTTCATTTCAATATATGTTGGCAAGCTAATATG 373

OY 249 TGATTCAGATTTGATGATATATCTCCACGACGTAAGGATGACGATGCCAGTTAC 308

DB 374 TGAAGAAAGATTTGGGTTTATCTCAAAATAAATGTGTTTAAATGTTGCTCTGTT 433

OY 309 CGGTATGCCCGTTCCCAAGCTTATTTCTTATTTAAAGCACTTGTAGTACCTTGA 368

DB 434 GTAGACATTTATTTGATATCAGTATCATCAATTAATTAATTTGATATTAATAA 493

OY 369 ACCAACACAAACACCTTAGAG 389

DB 494 AAAAAAAAAAAAACTCGAGG 514

RESULT 5

A2548969

LOCUS

DEFINITION ENTME27TF Entamoeba histolytica Sheared DNA Entamoeba histolytica

genomic, DNA sequence.

ACCESSION

A2548969

VERSION A2548969.1 GI:11173098

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Entamoeba histolytica.
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 911)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b1loftus@igf.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: Shotgun
High quality sequence start: 33
High quality sequence stop: 784.
Location/Qualifiers

FEATURES

source

1.911
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pROSI; Site_1: Bst I; Constructed at the
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.

BASE COUNT	519	a	49	c	200	g	143	e
ORIGIN								

Query Match	10.0%;	Score 39.2;	DB 17;	Length 480;
Best Local Similarity	84.6%;	Pred. No. 6.4;		
Matches 44;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;

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Qy      258 GATTGATGTGATATCTCCACTGACGTAAAGGATACGCATGCCAGTTACC 309
          |||||
Db      147 GATTGATGTGATATCTCCACTGACGTAAAGGATACGCACAATCCCCTATCC 96
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RESULT 7
BH751161

DEFINITION SALK_049464.49.75.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_049464.49.75.x, DNA sequence.

```

VERSION      BH751161.1  GI:18966302
KEYWORDS
SOURCE       GSS.
             thale cress.

```

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta,
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots,
Rosidae: eurosids II: Brassicales: Brassicaceae: Arabidopsis.

Alonso, J. M., Barajas, P., Chen, H., Cheuk, R., Gadrinab
 C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L., Shinn, P.,
 Zimmerman, J., and Ecker, J. R.

TITLE	LABORATORY OF INSECTION MODELS IN CMC
Accidence Inocced	
Arabadopsis Genome	
Unpublished (2001)	
Contact: Joseph R. Ecker	

Salk Institute Vennic Microanalysis Laboratory (559044)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752

fax: 030 256 0379
Email: eckerk@alk.edu
This is single pass sequence recovered from the left border of
TDNA.

```

Class: IDNA tagged.
FEATURES
  Location/Qualifiers
    1..112
    /organism="Arabidopsis thaliana"

```

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/clone_1b="Arabidopsis thaliana tRNA insertion 1b"
/clone="SALK_049464.49.75.x"
/db_xref="taxon:3702"
/strain="Columbia 0"

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/note-PCR was performed on Arabidopsis lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at

BASE COUNT 31 a 26 c 25 g 30 t

Query Match	9.9%	Score 39	DB 17	Length 112
Best Local Similarity	100.0%	Pred. No. 6		

QY 258 GATTGATGTATATCTCCACTGACGTAAAGGATGACCGCA 296
|||||

RESULT 8
BH749349
LOCUS
DEFINITION BH749349 142 bp DNA linear GSS 27-FEB-2002
SALK_047736.48.15.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_047736.48.15.x, DNA
sequence.
ACCESSION BH749349
VERSION BH749349
KEYWORDS BH749349.1 GI:18964144
GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 142)
Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
Source Location/Qualifiers
1..142
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_047736.48.15.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 41 a 36 c 30 g 35 t
ORIGIN
Query Match 9.9%; Score 39; DB 17; Length 142;
Best Local Similarity 100.0%; Pred. No. 6.2; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0;
QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCA 296
|||||
Db 33 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCA 71
RESULT 9
BH619283/c
LOCUS
DEFINITION BH619283 153 bp DNA linear GSS 30-JAN-2002
SALK_040762 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_040762, DNA sequence.
ACCESSION BH619283
VERSION BH619283
KEYWORDS BH619283.1 GI:18429799
GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 153)
Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab

,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
Source Location/Qualifiers
1..153
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_040762"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 36 a 34 c 36 g 47 t
ORIGIN
Query Match 9.9%; Score 39; DB 17; Length 153;
Best Local Similarity 100.0%; Pred. No. 6.3; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0;
QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCA 296
|||||
Db 110 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCA 72
RESULT 10
BH747013
LOCUS
DEFINITION BH747013 153 bp DNA linear GSS 27-FEB-2002
SALK_008070.43.05.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_008070.43.05.x, DNA
sequence.
ACCESSION BH747013
VERSION BH747013
KEYWORDS BH747013.1 GI:18960128
GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 153)
Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
Source Location/Qualifiers
1..153

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/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="SALK_008070.43.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna-protocols.html"

BASE COUNT      47 a      37 c      33 g      36 t

ORIGIN

Query Match      9.9%: Score 39; DB 17; Length 153;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 258 GATTGATGATATCTCCACTGACGTAGGATGACGCA 296
      |||||||
Db 44 GATTGATGATATCTCCACTGACGTAGGATGACGCA 82

RESULT 11
BH748291/c      158 bp      DNA      linear      GSS 27-FEB-2002
LOCUS      SALK_045100.51.10.x Arabidopsis thaliana TDNA insertion lines
DEFINITION      Arabidopsis thaliana genomic clone SALK_045100.51.10.x, DNA
sequence.
ACCESSION      BH748291
VERSION      BH748291.1 GI:18961648
KEYWORDS      GSS.
SOURCE      thale cress.
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1 (bases 1 to 158)
AUTHORS      Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE      A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL      Unpublished (2001)
COMMENT      Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
source      Location/Qualifiers
1..158
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
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/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna-protocols.html"

BASE COUNT      37 a      35 c      37 g      49 t

ORIGIN

Query Match      9.9%: Score 39; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 258 GATTGATGATATCTCCACTGACGTAGGATGACGCA 296
      |||||||
Db 110 GATTGATGATATCTCCACTGACGTAGGATGACGCA 72

RESULT 12
BH747357      165 bp      DNA      linear      GSS 27-FEB-2002
LOCUS      SALK_016522.55.50.x Arabidopsis thaliana TDNA insertion lines
DEFINITION      Arabidopsis thaliana genomic clone SALK_016522.55.50.x, DNA
sequence.
ACCESSION      BH747357
VERSION      BH747357.1 GI:18960472
KEYWORDS      GSS.
SOURCE      thale cress.
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1 (bases 1 to 165)
AUTHORS      Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE      A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL      Unpublished (2001)
COMMENT      Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
source      Location/Qualifiers
1..165
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
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/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna-protocols.html"

BASE COUNT      45 a      43 c      39 g      38 t

ORIGIN

Query Match      9.9%: Score 39; DB 17; Length 165;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 258 GATTGATGATATCTCCACTGACGTAGGATGACGCA 296
      |||||||
Db 34 GATTGATGATATCTCCACTGACGTAGGATGACGCA 72

RESULT 13
BH746616      175 bp      DNA      linear      GSS 27-FEB-2002
LOCUS      SALK_045268.54.50.x Arabidopsis thaliana TDNA insertion lines
DEFINITION      Arabidopsis thaliana genomic clone SALK_045268.54.50.x, DNA
sequence.
ACCESSION      BH746616
VERSION      BH746616.1 GI:18959731
KEYWORDS      GSS.
SOURCE      thale cress.
ORGANISM      Arabidopsis thaliana

```

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 175)

REFERENCE
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker

The Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

FEATURES

source

Location/Qualifiers

1..175

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_045268.54.50.x"

/note="PCR was performed on Arabidopsis thaliana lines"

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT 54 a 43 c 40 g 38 t

ORIGIN

Query Match 9.9%; Score 39; DB 17; Length 175;

Best Local Similarity 100.0%; Pred. No. 6.4;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCA 296

Db 66 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCA 104

RESULT 14
BH802465/c 177 bp DNA linear GSS 25-APR-2002

LOCUS 1008026E10.y2 1008 - Rescemu Grid 1 Zea mays genomic, DNA

DEFINITION sequence.

ACCESSION BH802465

VERSION BH802465.1 GI:20316614

KEYWORDS GSS.

SOURCE

ORGANISM

Zea mays.

Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 177)

REFERENCE

AUTHORS

Walbot,V.

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered Rescemu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site found so sequence was trimmed.

Post-ligation sequence submitted separately.

Class: transposon-tagged.

FEATURES

source

Location/Qualifiers

1..177

/organism="Zea mays"

/cultivar="mixed background W33/Al88/B73"

/db_xref="taxon:4577"

/clone_lib="1008 - Rescemu Grid 1"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: leaf; Vector: Rescemu (engineered from

pBluescript backbone); Site_1: BamHI; Site_2: BglII;

Rescemu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on Rescemu, go to the web

site www.zmld.laistate.edu and follow the links for

'Rescemu.' Grid 1 was grown at Berkeley in 2001. DNA was

extracted from leaf punches, double digested using BamHI

and BglII, and ligated to form circular plasmids. DH10B

cells were transformed and then screened on LB plates with

ampicillin."

39 a 38 c 47 g 53 t

BASE COUNT

ORIGIN

Query Match 9.9%; Score 39; DB 17; Length 177;

Best Local Similarity 100.0%; Pred. No. 6.4;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCA 296

Db 118 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCA 80

RESULT 15
BH752801 190 bp DNA linear GSS 27-FEB-2002

LOCUS SALK_019366.54.25.x Arabidopsis thaliana TDNA insertion lines

DEFINITION Arabidopsis thaliana genomic clone SALK_019366.54.25.x, DNA

sequence.

ACCESSION BH752801

VERSION BH752801.1 GI:18972023

KEYWORDS GSS.

SOURCE

ORGANISM

thale cress.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 190)

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,

C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,

Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

The Salk Institute Genomic Analysis Laboratory (SIGAL)

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

FEATURES

source

Location/Qualifiers

1..190

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_019366.54.25.x"

/note="PCR was performed on Arabidopsis thaliana lines"

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html.

BASE COUNT

52 a 52 c 41 g 45 t

ORIGIN

Query Match

9.9%; Score 39; DB 17; Length 190;

Best Local Similarity 100.0%; Pred. No. 6.4;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 296
|||||
Db 81 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 119

Search completed: April 14, 2003, 10:25:42
JOB time : 916.489 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 04:10:42 ; Search time 1319.64 Seconds

(without alignments)
10188.783 Million cell updates/sec

Title: US-09-963-803-20

Perfect score: 462
Sequence: 1 aagcttgatgcctgcagca.....cacacaactagagatcc 462

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Genem1:
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rod:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	100.0	462	6	AX036754
2	373.6	80.9	600	6	AX036756
3	364.6	78.9	9285	6	AX093047
4	364.6	78.9	15077	6	AX093052
5	354.2	76.7	541	6	AX036758
6	314	68.0	393	6	AX036753
7	262	56.7	604	6	AX036757
8	240.2	52.0	392	6	AX036755
9	212.4	46.0	317	6	AX036737
10	212.4	46.0	472	6	AX036759
11	200.4	43.4	348	6	AX036738
12	152.8	33.1	371	6	AX036739
13	140.8	30.5	301	6	AX036741
14	140.8	30.5	398	6	AX036740
15	120.6	26.1	515	6	AX036736
16	120.6	26.1	515	6	AX088388
17	120.6	26.1	532	6	AX020413
18	120.6	26.1	838	6	AX014764
19	120.6	26.1	853	6	AX088389
20	120.6	26.1	1036	6	AX014765
21	120.6	26.1	8158	14	CVU20341
22	120.6	26.1	8159	14	CVU59751
23	120.6	26.1	8340	6	AX329231
24	120.6	26.1	8340	6	AX338536
25	120.6	26.1	12241	6	AX412168
26	115.8	25.1	593	6	AX088390
27	115.8	25.1	857	6	AX088391
28	115.8	25.1	931	6	AX088392
29	115.4	25.0	931	6	AX088393
30	115.4	25.0	931	6	AX088393
31	81.4	17.6	7489	14	CYWVC8
32	80	17.3	243	6	AX036735
33	75.4	16.3	392	6	AX036755
34	69.6	15.1	79	6	AX036611
35	69.6	15.1	79	6	AX036748
36	69.6	15.1	296	6	AX036603
37	69	14.9	259	6	AX036616
38	62	13.4	60	6	AX036743
39	60	13.0	60	6	AX036746
40	60	12.6	80	6	AX103782
41	58	12.6	236	6	AX103783
42	58	12.6	299	6	AX103784
43	58	12.6	332	6	AX103755
44	58	12.6	472	6	AX103753
45	58	12.6	472	6	AX103753

ALIGNMENTS

RESULT 1
AX036754
LOCUS AX036754
DEFINITION Sequence 20 from Patent WO0058485.
ACCESSION AX036754
VERSION AX036754.1 GI:11226263
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 462)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 20 05-Oct-2000;
JOURNAL

MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
Location/Qualifiers
1. .462
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1163"

promoter
BASE COUNT 148 a 87 c 111 g 116 t
ORIGIN

Query Match 100.0%; Score 462; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.2e-116;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGCTTGATGCGCTGCAGCAGTATATCCGCGTCATCAATGACATCATCAGTACTGA 60
Db 1 AAGCTTGATGCGCTGCAGCAGTATATCCGCGTCATCAATGACATCATCAGTACTGA 60
Oy 61 GGAGTGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGAGCTAGCAGCAGC 120
Db 61 GGAGTGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGAGCTAGCAGCAGC 120
Oy 121 AACATGAAAGAAAGAAAGTAAAGTCGGTGAATGTAAGAGAGTAAAGAGTAAAGTAA 180
Db 121 AACATGAAAGAAAGAAAGTAAAGTCGGTGAATGTAAGAGAGTAAAGAGTAAAGTAA 180
Oy 181 AGGTGGAAGAAAGTAAAGGCGGAAAGTAACTTATGATTTGTAATTTGGTTACGACTAGT 240
Db 181 AGGTGGAAGAAAGTAAAGGCGGAAAGTAACTTATGATTTGTAATTTGGTTACGACTAGT 240
Oy 241 GATTGATGTGATATCAAGATTGATATCTCCACTGACGTAAGGATGACGATGCC 300
Db 241 GATTGATGTGATATCAAGATTGATATCTCCACTGACGTAAGGATGACGATGCC 300
Oy 301 ACGACTAGTGAATGATATCAAGATTGATATCTCCACTGACGTAAGGATGACGATGCC 360
Db 301 ACGACTAGTGAATGATATCAAGATTGATATCTCCACTGACGTAAGGATGACGATGCC 360
Oy 361 ACGTGGCAGCTTACCGCGTATGCCGTTATTCCTTATTTAATTTAAGCAGT 420
Db 361 ACGTGGCAGCTTACCGCGTATGCCGTTATTCCTTATTTAATTTAAGCAGT 420
Oy 421 GTGTAGTACCTTAGAAACCAACACACACACACACACCTAGAGATCC 462
Db 421 GTGTAGTACCTTAGAAACCAACACACACACACACACCTAGAGATCC 462

RESULT 2
AX036756 600 bp DNA linear PAT 16-NOV-2000

LOCUS AX036756
DEFINITION Sequence 22 from Patent WO0058485.
ACCESSION AX036756
VERSION AX036756.1 GI:11226265
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
1 (bases 1 to 600)

REFERENCE
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 22 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
JOURNAL
; GRUBER VERONIQUE (FR)
FEATURES
Location/Qualifiers
1. .600
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1165"

BASE COUNT 188 a 111 c 147 g 154 t
ORIGIN
promoter
188 a 111 c 147 g 154 t

Query Match 80.9%; Score 373.6; DB 6; Length 600;
Best Local Similarity 95.3%; Pred. No. 6e-92;
Matches 385; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Oy 1 AAGCTTGATGCGCTGCAGCAGTATATCCGCGTCATCAATGACATCATCAGTACTGA 60
Db 1 AAGCTTGATGCGCTGCAGCAGTATATCCGCGTCATCAATGACATCATCAGTACTGA 60
Oy 61 GGAGTGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGAGTAAAGAGTAAAGTAA 120
Db 61 GGAGTGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGAGTAAAGAGTAAAGTAA 120
Oy 121 AACATGAAAGAAAGAAAGTAAAGTCGGTGAATGTAAGAGAGTAAAGAGTAAAGTAA 180
Db 121 AACATGAAAGAAAGAAAGTAAAGTCGGTGAATGTAAGAGAGTAAAGAGTAAAGTAA 180
Oy 181 AGGTGGAAGAAAGTAAAGGCGGAAAGTAACTTATGATTTGTAATTTGGTTACGACTAGT 240
Db 181 AGGTGGAAGAAAGTAAAGGCGGAAAGTAACTTATGATTTGTAATTTGGTTACGACTAGT 240
Oy 241 GATTGATGTGATATCAAGATTGATATCTCCACTGACGTAAGGATGACGATGCC 300
Db 241 GATTGATGTGATATCAAGATTGATATCTCCACTGACGTAAGGATGACGATGCC 300
Oy 301 ACGACTAGTGAATGATATCAAGATTGATATCTCCACTGACGTAAGGATGACGATGCC 360
Db 301 ACGACTAGTGAATGATATCAAGATTGATATCTCCACTGACGTAAGGATGACGATGCC 360
Oy 361 ACGTGGCAGCTTACCGCGTATGCCGTTATTCCTTATTTAATTTAAGCAGT 404
Db 361 ACGTGGCAGCTTACCGCGTATGCCGTTATTCCTTATTTAATTTAAGCAGT 404

RESULT 3

AX093047 9285 bp DNA linear PAT 30-MAR-2001

LOCUS AX093047
DEFINITION Sequence 52 from Patent WO0118192.
ACCESSION AX093047
VERSION AX093047.1 GI:13509522
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
1 (bases 1 to 9285)

REFERENCE
AUTHORS Gruber, V. and Cemeu, D.
TITLE Synthetic vectors, transgenic plants containing them, and methods
for obtaining them
Patent: WO 0118192-A 52 15-MAR-2001;
JOURNAL
MERISTEM THERAPEUTICS (FR)
FEATURES
Location/Qualifiers
1. .9285
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PMR11336"

misc_feature
1
/note="PMR11336 results from the insertion into PMR1196
of the promoter MPr1165 isolated from plasmid PMR11322 as
described in PCT patent application PCT/IB00/00370"

BASE COUNT 2440 a 2252 c 2506 g 2087 t
ORIGIN

Query Match 78.9%; Score 364.6; DB 6; Length 9285;
Best Local Similarity 95.2%; Pred. No. 1.6e-89;
Matches 376; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Oy 10 TGCCTGCAGCACTATATCCGCGTCATCAATGACATCATCAGTACTGAGAGATGAA 69
Db 5799 TGCCTGCAGCACTATATCCGCGTCATCAATGACATCATCAGTACTGAGAGATGAA 5858
Oy 70 TAGCTAGCCATGACACTCTGTGCGAATATTGAAGAGCTAGACGACGACAAACATGAA 129
Db 5859 TAGCTAGCCATGACACTCTGTGCGAATATTGAAGAGCTAGACGACGACGACAAACATGAA 5918

OY 130 AAGAAGATTAAGGTCGATTTGTGAAGACATAGAGACATTAAGTGAAGAA 189
|||||
Db 5919 AAGAAGATTAAGGTCGATTTGTGAAGACATAGAGACATTAAGTGAAGAA 5978
OY 190 ATGAAGGCGGAAAGTAACCTATGCAATTTGTAATTTGGTTAGCACTAGTATGATGT 249
|||||
Db 5979 ATGAAGGCGGAAAGTAACCTATGCAATTTGTAATTTGGTTAGCACTAGTATGATGT 6038
OY 250 GATATCAAGATTGATGTATATCTCCACTGACGTAGAGGATGACGATGCCACTAGT 309
|||||
Db 6039 GATATCAAGATTGATGTATATCTCCACTGACGTAGAGGATGACGATGCCACTAGT 6098
OY 310 GATGATGTGATATCAAGATTGATGTATCTCCACTGACGTAGAGGATGACGATGCC 369
|||||
Db 6099 GATGATGTGATATCAAGATTGATGTATCTCCACTGACGTAGAGGATGACGATGCC 6158
OY 370 ACGTTACCGGTATGCCGTTCCCAAGCTTATTT 404
|||||
Db 6159 ACGACTAGTATGATGTATATCAAGATTGATGT 6193

RESULT 4
AX093052 15077 bp DNA linear PAT 30-MAR-2001
LOCUS Sequence 57 from Patent WO0118192.
DEFINITION AX093052
ACCESSION AX093052
VERSION AX093052.1 GI:13509527
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15077)
AUTHORS Gruber, V. and Comeau, D.
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them
JOURNAL Patent: WO 0118192-A 57 15-MAR-2001;
MERISTEM THERAPEUTICS (FR)
FEATURES
source location/Qualifiers
1..15077
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PMRT1342"
misc_feature 1
/note="PMRT1342 results from the replacement of the expression cassette ep355-gus-polyA35S from PMRT1335 by the expression cassette L5-gus-polyA35S isolated from PMRT1336"

BASE COUNT 3672 a 3892 c 4225 g 3288 t
ORIGIN

Query Match 78.9%; Score 364.6; DB 6; Length 15077;
Best Local Similarity 95.2%; Pred. NO. 1.5e-89;
Matches 376; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 10 TGGCTGAGCAGCTAGTATCCGCGTCATCATGACATCATACAGTACTGAGAGTGA 69
|||||
Db 6838 TGGCTGAGCAGCTAGTATCCCGTCATCATGACATCATACAGTACTGAGAGTGA 6897
OY 70 TAGTAGCCATGACACTCTGTGCAATATTTGAAGACGTAAACACTGACGACAAATGAA 129
|||||
Db 6898 TAGTAGCCATGACACTCTGTGCAATATTTGAAGACGTAAACACTGACGACAAATGAA 6957
OY 130 AAGAAGATTAAGTGGTGGTATTTGTGAAGACATAGAGACATGTAAGTGGAAA 189
|||||
Db 6958 AAGAAGATTAAGTGGTGGTATTTGTGAAGACATAGAGACATGTAAGTGGAAA 7017
OY 190 ATGAAGGCGGAAAGTAACCTATGCAATTTGTAATTTGGTTAGCACTAGTATGATGT 249
|||||
Db 7018 ATGAAGGCGGAAAGTAACCTATGCAATTTGTAATTTGGTTAGCACTAGTATGATGT 7077
OY 250 GATATCAAGATTGATGTATATCTCCACTGACGTAGAGGATGACGATGCCACTAGT 309
|||||

Db 7078 GATATCAAGATTGATGTATATCTCCACTGACGTAGAGGATGACGATGCCACTAGT 7137
OY 310 GATTGATGTGATATCAAGATTGATGTATATCTCCACTGACGTAGAGGATGACGATGCC 369
|||||
Db 7138 GATTGATGTGATATCAAGATTGATGTATATCTCCACTGACGTAGAGGATGACGATGCC 7197
OY 370 ACGTTACCGGTATGCCGTTCCCAAGCTTATTT 404
|||||
Db 7198 ACGACTAGTATGATGTATATCAAGATTGATGT 7232

RESULT 5
AX036758 541 bp DNA linear PAT 16-NOV-2000
LOCUS Sequence 24 from Patent WO058485.
DEFINITION AX036758
ACCESSION AX036758
VERSION AX036758.1 GI:11226267
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 541)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 24 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source location/Qualifiers
1..541
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter Mpri168"
BASE COUNT 169 a 104 c 130 g 138 t
ORIGIN

Query Match 76.7%; Score 354.2; DB 6; Length 541;
Best Local Similarity 98.4%; Pred. NO. 1.3e-86;
Matches 379; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

OY 78 CATGACACTGTGTCGAAATATTGAAGACGTAAACACTGACGACAAATGAAGAA 137
|||||
Db 160 CATGCACTGTGTGCAATATTGAAGACGTAAACACTGACGACAAATGAAGAA 219
OY 138 GATTAAGTGGTGTGTTGTAAGACATAGAGACATGTAAGTGGAAAATGTAAG 197
|||||
Db 220 GATTAAGTGGTGTGTTGTAAGACATAGAGACATGTAAGTGGAAAATGTAAG 278
OY 198 GCGGAAGTAACCTATGCAATTTGTAATTTGGTTAGCACTAGTATGATGTATCAA 257
|||||
Db 279 GCGGAAGTAACCTATGCAATTTGTAATTTGGTTAGCACTAGTATGATGTATCAA 338
OY 258 GATGATGTGATATCTCCACTGACGTAGAGGATGACGATGCCACTAGTATGATG 317
|||||
Db 339 GATGATGTGATATCTCCACTGACGTAGAGGATGACGATGCCACTAGTATGATG 398
OY 318 TGATATCAAGATTGATGTATATCTCCACTGACGTAGAGGATGACGATGCCACTAGT 377
|||||
Db 399 TGATATCAAGATTGATGTATATCTCCACTGACGTAGAGGATGACGATGCCACTAGT 458
OY 378 CCGTATGCCGTTCCCAAGCTTATTTGCTTATTTAAGCACTTGTAGTATGAAA 437
|||||
Db 459 CCGTATGCCGTTCCCAAGCTTATTTGCTTATTTAA - ACTGCTAGTATGCTTAA 516
OY 438 ACCAACAACAACCTAGAGATCC 462
|||||
Db 517 ACCAACAACAACCTAGAGATCC 541

RESULT 6
AX036753 393 bp DNA linear PAT 16-NOV-2000
LOCUS AX036753

DEFINITION Sequence 19 from Patent WO0058485.
ACCESSION AX036753
VERSION AX036753.1 GI:11226262
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .393
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MP1162"
BASE COUNT 128 a 75 c 93 g 97 t
ORIGIN
Query Match 68.0%; Score 314; DB 6; Length 393;
Best Local Similarity 85.1%; Pred. No. 1.5e-75;
Matches 393; Conservative 0; Mismatches 0; Indels 69; Gaps 1;
QY 1 AACCTGCAATGCTGAGCAGCTAGTATCCGCGTCATCATGATCATCATCACTACTGA 60
DB 1 AACCTGCAATGCTGAGCAGCTAGTATCCGCGTCATCATGATCATCATCACTACTGA 60
QY 61 GGAGATGAATAGCTAGCCATGACATCTGTGCGAATATTGAAGACCTAAGCAGCAG 120
DB 61 GGAGATGAATAGCTAGCCATGACATCTGTGCGAATATTGAAGACCTAAGCAGCAG 120
QY 121 AACAAATGAAAGAAAGATAGGTGGGTATGTGAAAGAGCATAGAGACATGTGA 180
DB 121 AACAAATGAAAGAAAGATAGGTGGGTATGTGAAAGAGCATAGAGACATGTGA 180
QY 181 AGGTGAAATGTAAGGCGGGAAGTAACTTATGCAATTTGTAATTTGGTTAGACTAG 240
DB 181 AGGTGAAATGTAAGGCGGGAAGTAACTTATGCAATTTGTAATTTGGTTAGACTAG 240
QY 241 GATTGATGTGATATCAAGATTGATGTATCTCAGCTGACGTAGAGGATGACGATGCC 300
DB 241 GATTGATGTGATATCAAGATTGATGTATCTCAGCTGACGTAGAGGATGACGATGCC 300
QY 301 ACAGCTAGCTATGATGTATATCAAGATTGATGTATCTCAGCTGACGTAGAGGATG 360
DB 301 ACAGCTAGCTATGATGTATATCAAGATTGATGTATCTCAGCTGACGTAGAGGATG 360
QY 361 ACAGCTAGCTATGATGTATATCAAGATTGATGTATCTCAGCTGACGTAGAGGATG 420
DB 361 ACAGCTAGCTATGATGTATATCAAGATTGATGTATCTCAGCTGACGTAGAGGATG 420
QY 421 GTGTAGTACCTTGAAGAACCAACAACCACTAGAGATCC 462
DB 421 GTGTAGTACCTTGAAGAACCAACAACCACTAGAGATCC 462
RESULT 7
AX036757 604 bp DNA linear PAT 16-NOV-2000
LOCUS AX036757
DEFINITION Sequence 23 from Patent WO0058485.
ACCESSION AX036757
VERSION AX036757.1 GI:11226266
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .392
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MP1164"
BASE COUNT 128 a 75 c 93 g 97 t
ORIGIN
Query Match 56.7%; Score 262; DB 6; Length 604;
Best Local Similarity 83.3%; Pred. No. 2.8e-61;
Matches 375; Conservative 0; Mismatches 5; Indels 70; Gaps 4;
QY 78 CATGACATCTGTGCGAATATTGAAGACCTAAGCAGCAGCAACATGAAAGAGAGA 137
DB 78 CATGACATCTGTGCGAATATTGAAGACCTAAGCAGCAGCAACATGAAAGAGAGA 137
QY 138 GATTAAGTGGTGTGTAAGAGACATAGAGGACATGTAAGTGGAAATGTAAGG 197
DB 138 GATTAAGTGGTGTGTAAGAGACATAGAGGACATGTAAGTGGAAATGTAAGG 197
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DB 220 GATTAAGTGGTGTGTAAGAGACATAGAGGACATGTAAGTGGAAATGTAAGG 278
QY 278 GCGAAGTAACTTATGCAATTTGTAATTTGTTAGCTAGTATGATGATATCA 257
DB 278 GCGAAGTAACTTATGCAATTTGTAATTTGTTAGCTAGTATGATGATATCA 257
QY 258 GATTGATGTGATATCTCCACTGACGTAGAGGATGACGATGCCA 301
DB 258 GATTGATGTGATATCTCCACTGACGTAGAGGATGACGATGCCA 301
QY 337 GATTGATGTGATATCTCCACTGACGTAGAGGATGACGATGCCA 366
DB 337 GATTGATGTGATATCTCCACTGACGTAGAGGATGACGATGCCA 366
QY 302 CGACTAGTAT 312
DB 397 ATATCAAGTTGATGTATATCTCCACTGACGTAGAGGATGACGATGCCA 456
QY 313 TGATGTGATATCAAGATTGATGTATCTCCACTGACGTAGAGGATGACGATGCCA 372
DB 457 TGATGTGATATCAAGATTGATGTATCTCCACTGACGTAGAGGATGACGATGCCA 372
QY 373 TTAACCGGTATGCGGTTCCCAAGCTTTATTTCTTATTTAAGCACTTTGATAGCTT 432
DB 517 TTAACCGGTATGCGGTTCCCAAGCTTTATTTCTTATTTAAGCACTTTGATAGCTT 432
QY 433 AGAAGCAACAACCAACCACTAGAGATCC 462
DB 575 AGAAGCAACAACCAACCACTAGAGATCC 604
RESULT 8
AX036755 392 bp DNA linear PAT 16-NOV-2000
LOCUS AX036755
DEFINITION Sequence 21 from Patent WO0058485.
ACCESSION AX036755
VERSION AX036755.1 GI:11226264
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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source
1. .392
/organism="synthetic construct"
/db_xref="taxon:32630"
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BASE COUNT 128 a 75 c 93 g 97 t
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Query Match 56.7%; Score 262; DB 6; Length 604;
Best Local Similarity 83.3%; Pred. No. 2.8e-61;
Matches 375; Conservative 0; Mismatches 5; Indels 70; Gaps 4;
QY 78 CATGACATCTGTGCGAATATTGAAGACCTAAGCAGCAGCAACATGAAAGAGAGA 137
DB 78 CATGACATCTGTGCGAATATTGAAGACCTAAGCAGCAGCAACATGAAAGAGAGA 137
QY 138 GATTAAGTGGTGTGTAAGAGACATAGAGGACATGTAAGTGGAAATGTAAGG 197
DB 138 GATTAAGTGGTGTGTAAGAGACATAGAGGACATGTAAGTGGAAATGTAAGG 197
QY 220 GATTAAGTGGTGTGTAAGAGACATAGAGGACATGTAAGTGGAAATGTAAGG 278
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QY 278 GCGAAGTAACTTATGCAATTTGTAATTTGTTAGCTAGTATGATGATATCA 257
DB 278 GCGAAGTAACTTATGCAATTTGTAATTTGTTAGCTAGTATGATGATATCA 257
QY 258 GATTGATGTGATATCTCCACTGACGTAGAGGATGACGATGCCA 301
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QY 302 CGACTAGTAT 312
DB 397 ATATCAAGTTGATGTATATCTCCACTGACGTAGAGGATGACGATGCCA 456
QY 313 TGATGTGATATCAAGATTGATGTATCTCCACTGACGTAGAGGATGACGATGCCA 372
DB 457 TGATGTGATATCAAGATTGATGTATCTCCACTGACGTAGAGGATGACGATGCCA 372
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DB 517 TTAACCGGTATGCGGTTCCCAAGCTTTATTTCTTATTTAAGCACTTTGATAGCTT 432
QY 433 AGAAGCAACAACCAACCACTAGAGATCC 462
DB 575 AGAAGCAACAACCAACCACTAGAGATCC 604

JOURNAL
PATENT: WO 0058485-A 23 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
LOCATION/Qualifiers
1. .604
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MP1167"
BASE COUNT 186 a 116 c 145 g 157 t
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Query Match 56.7%; Score 262; DB 6; Length 604;
Best Local Similarity 83.3%; Pred. No. 2.8e-61;
Matches 375; Conservative 0; Mismatches 5; Indels 70; Gaps 4;
QY 78 CATGACATCTGTGCGAATATTGAAGACCTAAGCAGCAGCAACATGAAAGAGAGA 137
DB 78 CATGACATCTGTGCGAATATTGAAGACCTAAGCAGCAGCAACATGAAAGAGAGA 137
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DB 138 GATTAAGTGGTGTGTAAGAGACATAGAGGACATGTAAGTGGAAATGTAAGG 197
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DB 278 GCGAAGTAACTTATGCAATTTGTAATTTGTTAGCTAGTATGATGATATCA 257
QY 258 GATTGATGTGATATCTCCACTGACGTAGAGGATGACGATGCCA 301
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QY 302 CGACTAGTAT 312
DB 397 ATATCAAGTTGATGTATATCTCCACTGACGTAGAGGATGACGATGCCA 456
QY 313 TGATGTGATATCAAGATTGATGTATCTCCACTGACGTAGAGGATGACGATGCCA 372
DB 457 TGATGTGATATCAAGATTGATGTATCTCCACTGACGTAGAGGATGACGATGCCA 372
QY 373 TTAACCGGTATGCGGTTCCCAAGCTTTATTTCTTATTTAAGCACTTTGATAGCTT 432
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QY 433 AGAAGCAACAACCAACCACTAGAGATCC 462
DB 575 AGAAGCAACAACCAACCACTAGAGATCC 604
RESULT 8
AX036755 392 bp DNA linear PAT 16-NOV-2000
LOCUS AX036755
DEFINITION Sequence 21 from Patent WO0058485.
ACCESSION AX036755
VERSION AX036755.1 GI:11226264
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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/organism="synthetic construct"
/db_xref="taxon:32630"
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BASE COUNT 128 a 75 c 93 g 97 t
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Best Local Similarity 83.3%; Pred. No. 2.8e-61;
Matches 375; Conservative 0; Mismatches 5; Indels 70; Gaps 4;
QY 78 CATGACATCTGTGCGAATATTGAAGACCTAAGCAGCAGCAACATGAAAGAGAGA 137
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QY 278 GCGAAGTAACTTATGCAATTTGTAATTTGTTAGCTAGTATGATGATATCA 257
DB 278 GCGAAGTAACTTATGCAATTTGTAATTTGTTAGCTAGTATGATGATATCA 257
QY 258 GATTGATGTGATATCTCCACTGACGTAGAGGATGACGATGCCA 301
DB 258 GATTGATGTGATATCTCCACTGACGTAGAGGATGACGATGCCA 301
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DB 337 GATTGATGTGATATCTCCACTGACGTAGAGGATGACGATGCCA 366
QY 302 CGACTAGTAT 312
DB 397 ATATCAAGTTGATGTATATCTCCACTGACGTAGAGGATGACGATGCCA 456
QY 313 TGATGTGATATCAAGATTGATGTATCTCCACTGACGTAGAGGATGACGATGCCA 372
DB 457 TGATGTGATATCAAGATTGATGTATCTCCACTGACGTAGAGGATGACGATGCCA 372
QY 373 TTAACCGGTATGCGGTTCCCAAGCTTTATTTCTTATTTAAGCACTTTGATAGCTT 432
DB 517 TTAACCGGTATGCGGTTCCCAAGCTTTATTTCTTATTTAAGCACTTTGATAGCTT 432
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DB 575 AGAAGCAACAACCAACCACTAGAGATCC 604

BASE COUNT	127 a	80 c	87 g	98 t		
ORIGIN						
Query Match	52.0%; Score 240.2; DB 6; Length 392;					
Best Local Similarity	77.4%; Pred. No. 2.8e-55;					
Matches 349; Conservative	0; Mismatches 33; Indels 69; Gaps 2;					
OY	1	AAGCTTGCACTGCTTCACGACCTAGTATCGCCGCTATCATATCATATCATATGACTGCA	60			
DB	1	AAGCTTGCACTGCTTCACGACCTAGTATCGCCGCTATCATATCATATCATATGACTGCA	60			
OY	61	GGAGATGATAGCTAGCTGACCTGACCTGCTGCGGATTTTGAAGACGTAAAGCATGACGAC	120			
DB	61	GGAGATGATAGCTAGCTGACCTGACCTGCTGCGGATTTTGAAGACGTAAAGCATGACGAC	120			
OY	121	AACCAATGAAAAGAAAGATTAAGTCTGGTATTTGAAAGAGACATAGAGACATGTA	180			
DB	121	AACCAATGAAAAGAAAGATTAAGTCTGGTATTTGAAAGAGACATAGAGACATGTA	180			
OY	181	AGGTGGAATAATTAAGGCGGGAAGTAACCTTATTCATTTGTAATTTGGTTACGACTAGT	240			
DB	181	AGGTGGAATAATTAAGGCGGGAAGTAACCTTATTCATTTGTAATTTGGTTACGACTAGT	240			
OY	241	GATTGATGATGATCAAGATTGATGATATTCACAGCTAAGGATGACGATGCC	300			
DB	241	GATTGATGATGATCAAGATTGATGATATTCACAGCTAAGGATGACGATGCC	300			
OY	301	ACGACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	360			
DB	251	TTAGCTCAGTGGAGATATCATCATCATATCTGATATCATCATC-----	291			
OY	361	ACGCAATGCCACGCTTAACCCGGTATGCGCGGTCCCAAGCTTTATTTCCCTTAATTAACGACT	420			
DB	292	AATCACTAGTGTGTTACCCGGTATGCGCGGTCCCAAGCTTTATTTCCCTTAATTAACGACT	351			
OY	421	GGTGTAGTACTTAGAAAACCAACCAACAAC	451			
DB	352	GGTGTAGTACTTAGAAAACCAACCAACAAC	382			
RESULT 9						
LOCUS	AX036737	317 bp	DNA	linear		
DEFINITION	Sequence 3 from Patent WO058485.					
ACCESSION	AX036737					
VERSION	AX036737.1	GI:11226246				
KEYWORDS	.					
SOURCE	synthetic construct.					
ORGANISM	synthetic construct.					
REFERENCE	1 (bases 1 to 317)					
AUTHORS	Rance, I., Theisen, M. and Gruber, V.					
TITLE	Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus					
JOURNAL	Patent: WO 0058485-A 3 05-Oct-2000;					
FEATURES	MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)					
source	; GRUBER VERONIQUE (FR)					
	Location/Qualifiers					
	1..317					
	/organism="synthetic construct"					
	/db_xref="taxon:32630"					
	/note="Promoter MPrill16"					
Promoter	1..317					
BASE COUNT	107 a	61 c	74 g	75 t		
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Query Match	46.0%; Score 212.4; DB 6; Length 317;					
Best Local Similarity	99.5%; Pred. No. 1.2e-47;					
Matches 213; Conservative	0; Mismatches 1; Indels 0; Gaps 0;					
OY	20	ACTGATATCCCGCCGATCAATGATCATATCATAGTATGAGAGATGAATAGCTAGCA	79			
DB	18	ACTGATATCCCGCCGATCAATGATCATATCATAGTATGAGAGATGAATAGCTAGCA	77			

LOCUS	SEQUENCE	FROM	PATENT	NOV-2000
LOCUS	AX036738	348 bp	DNA	linear
DEFINITION	Sequence 4 from Patent WO0058485.			
ACCESSION	AX036738			
VERSION	AX036738.1	GI:11226247		
KEYWORDS	synthetic construct.			
FEATURES				
SOURCE	location/Qualifiers			
	1..472			
	/organism="synthetic construct"			
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PROMOTER	1..472			
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Query Match	46.0%, Score 212.4; DB 6; Length 472;			
Best Local Similarity	91.5%; Pred. No. 1.2e-47;			
Matches 236; Conservative	0; Mismatches 21; Indels 1; Gaps 1;			
QY	78 CATGACTCTGCTGGGATATTTGAAGACGTAAAGCACTACGACACACATGAAAGAAAGAA 137			
DB	160 CATGCACTCTGCTGGGATATTTGAAGACGTAAAGCACTACGACACACATGAAAGAAAGAA 219			
QY	138 GATAAGTCGGTGATTTGAAAGAGACATTAAGACACATGTAAGTGGAAATGTAAGG 197			
DB	220 GATAAGTCGGTGATTTGAAAGAGACATTAAGACACATGTAAGTGGAAATGTAAGG 278			
QY	198 GCGGAAGTAACTTATGCAATTTGTAATTTGGTTACGACTAGTGTGATATCA 257			
DB	279 GCGGAAGTAACTTATGCAATTTGTAATTTGGTTACGACTAGTGTGATATCA 338			
QY	258 GATTGATGTGATATTCACAGACGTAAAGGATGAGCATGACACATAGATGATTATG 317			
DB	339 GATTGATGTGATATTCACAGACGTAAAGGATGAGCATGACACATAGATGATTATG 398			
QY	318 TGATATCAAGATGTATGT 335			
DB	399 GGTTCACCAAGCTTATTT 416			
RESULT 11				
LOCUS	AX036738	348 bp	DNA	linear
DEFINITION	Sequence 4 from Patent WO0058485.			
ACCESSION	AX036738			
VERSION	AX036738.1	GI:11226247		
KEYWORDS	synthetic construct.			

ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 348)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 4 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
FEATURES
LOCATION/Qualifiers
SOURCE 1..348
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1117"
Promoter 1..348
BASE COUNT 116 a 70 c 78 g 84 t
ORIGIN
Query Match 43.4%; Score 200.4; DB 6; Length 348;
Best Local Similarity 99.1%; Pred. No. 2.4e-44;
Matches 212; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 20 ACTAGATCGCGGTCATCATGATCATCATGAGAGATGTAATGCTAGCCA 79
Db 52 ACTAGATCGCGGTCATCATGATCATCATGAGAGATGTAATGCTAGCCA 111
QY 80 TGACACTCTGTGCGAATATTGAAGACGTAGCAGCAACAATGAAGAAGAA 139
Db 112 TGACACTCTGTGCGAATATTGAAGACGTAGCAGCAACAATGAAGAAGAA 171
QY 140 TTAGGTGGTGTATTGTAAGACATAGAGACACATGTAAGTGAATGTAAAGGC 199
Db 172 TTAGGTGGTGTATTGTAAGACATAGAGACACATGTAAGTGAATGTAAAGGC 230
QY 200 GGAAAGTAACTTATGATTTGTAATTTGTTAC 233
Db 231 GGAAAGTAACTTATGATTTGTAATTTGTTAC 264
RESULT 12
LOCUS AX036739 371 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 5 from Patent WO0058485.
ACCESSION AX036739
VERSION AX036739.1 GI:11226248
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 371)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 5 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
FEATURES
LOCATION/Qualifiers
SOURCE 1..371
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1146"
Promoter 1..371
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ORIGIN
Query Match 33.1%; Score 152.8; DB 6; Length 371;
Best Local Similarity 98.7%; Pred. No. 2.9e-31;
Matches 154; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 78 CATGACACTCTGTGCGAATATTGAAGACGTAGCAGCAACAATGAAGAAGAA 137
Db 130 CATGACACTCTGTGCGAATATTGAAGACGTAGCAGCAACAATGAAGAAGAA 189

QY 138 GATAAGTCGTGATTTGTAAGACATAGAGACATGTAAGTGGAATGTAAAG 197
Db 190 GATAAGTCGTGATTTGTAAGACATAGAGACATGTAAGTGGAATGTAAAG 249
QY 198 GCGGAAGTAACTTATGATTTGTAATTTGTTAC 233
Db 250 GCGGAAGTAACTTATGATTTGTAATTTGTTAC 285
RESULT 13
LOCUS AX036741 301 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 7 from Patent WO0058485.
ACCESSION AX036741
VERSION AX036741.1 GI:11226250
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 301)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 7 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
FEATURES
LOCATION/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1154"
Promoter 1..301
BASE COUNT 98 a 54 c 74 g 75 t
ORIGIN
Query Match 30.5%; Score 140.8; DB 6; Length 301;
Best Local Similarity 98.1%; Pred. No. 5.7e-28;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 78 CATGACACTCTGTGCGAATATTGAAGACGTAGCAGCAACAATGAAGAAGAA 137
Db 63 CATGACACTCTGTGCGAATATTGAAGACGTAGCAGCAACAATGAAGAAGAA 122
QY 138 GATAAGTCGTGATTTGTAAGACATAGAGACATGTAAGTGGAATGTAAAG 197
Db 123 GATAAGTCGTGATTTGTAAGACATAGAGACATGTAAGTGGAATGTAAAG 181
QY 198 GCGGAAGTAACTTATGATTTGTAATTTGTTAC 233
Db 182 GCGGAAGTAACTTATGATTTGTAATTTGTTAC 217
RESULT 14
LOCUS AX036740 398 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 6 from Patent WO0058485.
ACCESSION AX036740
VERSION AX036740.1 GI:11226249
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 398)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 6 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
FEATURES
LOCATION/Qualifiers
SOURCE 1..398
/organism="synthetic construct"
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10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
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12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT.*
17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*
19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2004.DAT.*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2005.DAT.*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2006.DAT.*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2007.DAT.*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2008.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2009.DAT.*

```

SUMMARIES

Description	Amount
...	...

Result	Score	% Match	Query Length	DB ID	Nucleotide sequence
1	462	100.0	462	AAA96854	Nucleotide sequenc
2	462	100.0	462	AAA96856	Nucleotide sequenc
3	462	100.0	462	AAA96858	Nucleotide sequenc
4	462	100.0	462	AAA96855	Nucleotide sequenc
5	462	100.0	462	AAA96857	Nucleotide sequenc
6	462	100.0	462	AAA96858	Nucleotide sequenc
7	462	100.0	462	AAA96853	Nucleotide sequenc

10	152.8	33.1	371.1	21	AAA96839
11	140.8	30.5	398.21	21	AAA96840
12	120.6	26.1	392.19	19	AAV14013
13	120.6	26.1	411.1	19	AAV14016
14	120.6	26.1	515.22	22	AAA96805
15	120.6	26.1	515.22	22	AAE53020
16	120.6	26.1	524.19	19	AAV14018
17	120.6	26.1	526.22	22	AAV15755
18	120.6	26.1	533.22	22	AAE55506
19	120.6	26.1	933.22	22	AAV15988
20	120.6	26.1	1839.24	24	AB157982
21	120.6	26.1	1677.24	24	AB158005
22	120.6	26.1	8187.24	24	ABE04139
23	120.6	26.1	8340.24	24	ABD21049
24	120.6	26.1	8340.24	24	ABD16732
25	120.6	26.1	12241.19	19	AAV14026
26	120.6	26.1	12245.19	19	AAV14026
27	117.4	25.4	320.19	19	AAV14052
28	117.4	25.4	476.19	19	AAV14057
29	117.4	25.4	593.22	22	AAE55508
30	115.8	25.1	857.22	22	AAE55209
31	115.8	25.1	931.22	22	AAE55510
32	115.8	25.1	931.22	22	AAE55510
33	115.4	25.0	931.19	19	AAV14027
34	115.4	25.0	931.19	19	AAV14032
35	81.8	17.5	481.19	19	AAA96835
36	80	17.3	443.21	21	AAA96835
37	79.6	16.3	491.19	19	AAV14035
38	79.6	16.3	392.21	21	AAA96823
39	75.4	16.0	261.21	21	AAV14848
40	69.6	15.1	79.21	21	AAA96472
41	69.6	15.1	29.21	21	AAA96655
42	69.6	15.1	29.21	21	AAA96647
43	69.6	15.1	29.21	21	
44	69.6	15.1	29.21	21	
45	69.6	15.1	29.21	21	

ALIGNMENTS

[illegible]

RESULT 1
XX
AA096854 standard; DNA:
ID AA096854
XX AAA06054: (first entry)
XX 19-FEB-2001
DT Nucleotide sequence of chimeric expression promoter;
DE intergenic region; Commelina yellow mottle virus;
DE intergenic promoter; plant vascular expression promoter; Cassava vein mosaic virus
XX Promoter; intergenic expression promoter;
XX chimeric green tissue expression promoter; ss.
KM plant green tissue chimera; ss.
KM transgenic plant; yellow mottle virus.
KW Transgenic - Commelina yellow mottle virus.
XX Chimeric - Cassava vein mosaic virus.
XX Chimeric
OS
XX WO200058485-A1.
PN 05-OCT-2000.
XX 29-MAR-2000; 2000WO-IB00370.
PD 99FR-0003925.
XX 29-MAR-1999;
PE MERISTEM THERAPEUTICS.
XX (MERI-) Gruber V., Thøgersen M;
XX Rance I,
XX PI WPI: 2000-647218/62.
XX DR

MP1168.
bottle virus;
expression promoter;
vein mosaic virus;

[illegible]

CC promoter region. Preferably, the first plant promoter originates from
CC Comelina yellow mottle virus, and the second plant promoters are
CC from the Cassava vein mosaic virus. Especially, the chimeric promoters are
CC derived from intergenic regions. The chimeric promoters are used
CC for producing transgenic plants.

XX Sequence 604 BP; 186 A; 116 C; 145 G; 157 T; 0 other;

SQ

Query Match 56.7%; Score 262; DB 21; Length 604;
Best Local Similarity 83.3%; Pred. No. 2.7e-70; Indels 70; Gaps
Matches 375; Conservative 0; Mismatches 5;

DG
GTATGACCTCTTGGCAGATATTGGANAGACGTAAACACTGACGCACCAATGAAGAAGAA 219
|||||
DQ 160 CATGCCACTCTGTGCGAATTTTCAGACGTAAAGCATGACCTGACGCACCAATGAAGAAGAA 219
|||||
DY 78 CATGACCTCTTGGCAGATATTGGANAGACGTAAACACTGACGCACCAATGAAGAAGAA 219
|||||
DB 160 CATGCCACTCTGTGCGAATTTTCAGACGTAAAGCATGACCTGACGCACCAATGAAGAAGAA 219
|||||
DY 138 GATTAAGTCGGTGATGTGGAAGAGACATAGAGACACATGTAAGTGGAAATGTAGG 278
|||||
DY 220 GATAAGTCGGTGATGTGGAAGAGACATAGAGACACATGTAAGTGGAAATGTAGG 278
|||||
DB 198 GCGGAAATACCTTTATGCAATTTGTAATTTGGTACAGTAGATGATGATATCAA 336
|||||
DY 279 GCGGAAATACCTTTATGCAATTTGTAATTTGGTACAGTAGATGATGATATCAA 336
|||||
DB 258 GATTGATGATATATCTCCATGACGTAAAGGATAGACCATGCA 301
|||||
DY 337 GATTGATGATATATCTCCATGACGTAAAGGATAGACCATGCA 301
|||||
DB 302 ----- CGACTGTGAT 312
|||||
DY 397 ATATCAAGATGATGATATCTCCATGACGTAAAGGATAGACCATGCA 312
|||||
DB 397 ATATCAAGATGATGATATCTCCATGACGTAAAGGATAGACCATGCA 312
|||||

[illegible]

RESULT 6
... 392 BP.

AC
XX
XX
XX
DT
XX
XX
XX
KW
KW
KW
KW
XX

Annals
19-FEB-2001 (first entry)

Nucleotide sequence of chimeric expression promoter MpR16d.

Intergenic region; Commelina yellow mottle virus;
Promoter: intergenic promoter; plant vascular expression mosaic virus
chimeric expression promoter; Cassava vein mosaic virus
plant green tissue expression promoter; ss.
transgenic plant; chimera; ss.
Chimeric - Commelina yellow mottle virus.
Cassava vein mosaic virus.

XX WO200058485-A1.
PN
XX 05-OCT-2000.
PD
XX 29-MAR-2000; 2000WO-IB00370
PP

AA 29-MAR-1999;
PR
XX (MERT-) MERISTEM THERAPEUTICS
PA
XX

PI	Rance I, Gruber V, Theisen M,	
XX	WPI: 2000-647238/62.	
XX		
PT	Chimeric expression promoter for transgenic plant production, comprises	
PT	sequence from promoter comprising vascular expression region replaced	
PT	with sequence from promoter comprising green tissue expression region	
PT		
XX	Claim 5; Page 86; 91pp; English.	
PS		
XX		
CC	The present sequence represents a chimeric promoter of the invention.	
CC	The specification describes chimeric expression promoters. These	
CC	chimeric promoters comprise a nucleic acid sequence which is derived	
CC	from a first plant promoter, in which a plant vascular expression	
CC	promoter region is replaced with a nucleic acid sequence derived from	
CC	a second plant promoter comprising a plant green tissue expression	
CC	promoter region. Preferably, the first plant promoter originates from	
CC	Commelina yellow mottle virus, and the second plant promoter originates	
CC	from the Cassava vein mosaic virus. Especially, the promoters are	
CC	derived from intergenic regions. The chimeric promoters are useful	
CC	for producing transgenic plants.	
XX		
S0	Sequence 392 BP; 127 A; 80 C; 87 G; 98 T; 0 other;	
	Query Match 52.0%; Score 240.2; DB 21; Length 392;	
	Best Local Similarity 77.4%; Pred. No. 1.1e-63;	
	Matches 349; Conservative 0; Mismatches 33; Indels 69; Gaps	
OY	1 AAGCTTGACGCTCCAGCAGCTAGTATCCGCCGTATCATCATGACATCAGTACTCA 60	
DB	1 AAGCTTGACGCTCCAGCAGCTAGTATCCGCCGTATCATCATGACATCAGTACTCA 60	
OY	61 GGAGATGATAGCTTACGCTGACACTCTGTGGGAATATTGAAGACGTAGACACTGACGAC 120	
DB	61 GGAGATGATAGCTTACGCTGACACTCTGTGGGAATATTGAAGACGTAGACACTGACGAC 120	
OY	121 AACCAATGAAAAGAGAGATTAAGTTCGTGATTGTGAAAAGACATAGAGACATGTGA 180	
DB	121 AACCAATGAAAAGAGAGATTAAGTTCGTGATTGTGAAAAGACATAGAGACATGTGA 180	
OY	181 AGGTGGAAATTTAAGGGCGGAAAGTAACCTTATGATTTGTAATTTGGTTACGACTAGT 240	
DB	181 AGGTGGAAATTTAAGGGCGGAAAGTAACCTTATGATTTGTAATTTGGTTACGACTAGT 240	
OY	241 GATTGATGTGATATCAAGATTGATGTGATATCTCACATGACGTAAAGGATGACGATGCC 300	
DB	241 GATTGATGTGATATCAAGATTGATGTGATATCTCACATGACGTAAAGGATGACGATGCC 300	
OY	301 ACGACTAGTGTGATGTGATATCAAGATTGATGTGATATCTCAACTGACGTAAAGGATG 360	
DB	301 ACGACTAGTGTGATGTGATATCAAGATTGATGTGATATCTCAACTGACGTAAAGGATG 360	
OY	361 ACGCATGCCAGCTTACCCGGTATGCCGGTTCGCCAAGCTTATTTCTTATTTAAGCATT 420	
DB	361 ACGCATGCCAGCTTACCCGGTATGCCGGTTCGCCAAGCTTATTTCTTATTTAAGCATT 420	
OY	421 GTGTAGTACTTAGAAAACACACACAAAC 451	
DB	421 GTGTAGTACTTAGAAAACACACACAAAC 451	
	352 GTGTAGTACTTAGAAAACACACAAAC 382	
RESULT 7		
ID	AAA96837	
XX	AAA96837 standard; DNA; 317 BP.	
XX	AAA96837;	
XX	19-FEB-2001 (first entry)	
XX		
DE	Nucleotide sequence of chimeric expression promoter MP1116.	
XX		
XX	Promoter; intergenic region; Commelina yellow mottle virus;	

Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
QY 20 ACTAGTATCCGCCGCGTCATCATGACATATCATCTACAGTACTGAGAGAGATGATAGCTAGGCA 79	46.0%; Score 212.4; DB 21; Length 317;	213;	0;	1;	0;	0;
DB 18 ACTAGTATCCGCCGCGTCATCATGACATATCATCTACAGTACTGAGAGAGATGATAGCTAGGCA 77	49.5%; Pred. No. 3.4e-55;	213;	0;	1;	0;	0;
QY 80 TGACACTCTGTGTCGCAATATTGTAAGACGTAGACAGCAGCAACAATGAAAAAGAGA 139		213;	0;	1;	0;	0;
DB 78 TGACACTCTGTGTCGCAATATTGTAAGACGTAGACAGCAGCAACAATGAAAAAGAGA 137		213;	0;	1;	0;	0;
QY 140 TAAGTCGCGTGTATTGTAAGAGACATAGAGACACATGTAAAGTGAAGAAATGTAAGGC 199		213;	0;	1;	0;	0;
DB 138 TAAGTCGCGTGTATTGTAAGAGACATAGAGACACATGTAAAGTGAAGAAATGTAAGGC 197		213;	0;	1;	0;	0;
QY 200 GGAAGTAACCTTATGACATTTGTAATTTGGTTAC 233		213;	0;	1;	0;	0;
DB 198 GGAAGTAACCTTATGACATTTGTAATTTGGTTAC 231		213;	0;	1;	0;	0;
RESULT 8						
ID AAA96859 standard; DNA: 472 BP.						
XX AAA96859;						
XX 19-FEB-2001 (first entry)						
XX Nucleotide sequence of chimeric expression promoter MPR1169.						

```
KM Promoter; intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
PN WO200058485-A1.
XX
XX 05-OCT-2000.
PD
XX 29-MAR-2000; 2000WO-IB00370.
PE
XX 29-MAR-1999; 99FR-0003925.
PR
XX (MERI-) MERISTEM THERAPEUTICS.
PA
XX Rance I, Gruber V, Theisen M;
PI
XX WPI; 2000-647238/62.
DR
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX
XX Claim 5; Page 88; 91pp; English.
PS
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
CC
XX
XX Sequence 472 BP; 149 A; 92 C; 112 G; 119 T; 0 other;
SQ
Query Match 46.0%; Score 212.4; DB 21; Length 472;
Best Local Similarity 91.5%; Pred. No. 4e-55;
Matches 236; Conservative 0; Mismatches 21; Indels 1; Gaps 1;
OY 78 CATGACACTCTGCGCAATATTGAGACGTAAGCACTGACGACAAACAATGAAAGAA 137
DB 160 CATGCCACTGTGCGCAATATTGAGACGTAAGCACTGACGACAAACAATGAAAGAA 219
OY 138 GATAAGGTCGGTATTGTGAAAGACATAGAGACACATGTAAGTGAATAAG 197
DB 220 GATAAGGTCGGTATTGTG- AAGACATAGAGACACATGTAAGTGAATAAG 278
OY 198 GCGGAAGTAACCTTATGCACTTTGTAATTGGTTAGCAGTATGATGATATCAA 257
DB 279 GCGGAAGTAACCTTATGCACTTTGTAATTGGTTAGCAGTATGATGATATCAA 338
OY 258 GATTGATGATATTCACATGAGCAGTAAGGATGAGCAGCAGCAGCTATGATGATG 317
DB 339 GATTGATGATATTCACATGAGCAGTAAGGATGAGCAGCAGCAGCTATGATGATG 398
OY 318 TGATATCAAGATTGATGT 335
DB 399 GGTTCACCAAGCTTATTT 416
RESULT 9
AAA96838
ID AAA96838 standard; DNA; 348 BP.
XX
AC AAA96838;
```

```
XX
XX 19-FEB-2001 (first entry)
DT
XX Nucleotide sequence of chimeric expression promoter MPR117.
DE
XX
XX Promoter; intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
XX Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
OS
PN WO200058485-A1.
XX
XX 05-OCT-2000.
PD
XX 29-MAR-2000; 2000WO-IB00370.
PE
XX 29-MAR-1999; 99FR-0003925.
PR
XX (MERI-) MERISTEM THERAPEUTICS.
PA
XX Rance I, Gruber V, Theisen M;
PI
XX WPI; 2000-647238/62.
DR
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX
XX Claim 5; Page 81; 91pp; English.
PS
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
CC
XX
XX Sequence 348 BP; 116 A; 70 C; 78 G; 84 T; 0 other;
SQ
Query Match 43.4%; Score 200.4; DB 21; Length 348;
Best Local Similarity 99.1%; Pred. No. 1.7e-51;
Matches 212; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 20 ACTAGTATCGCGCGTATCATGACATCATCAGTACTGAGGAGATGAACTAGCA 79
DB 52 ACTAGTATCGCGCGTATCATGACATCATCAGTACTGAGGAGATGAACTAGCA 111
OY 80 TGACACTCTGTGCGCAATATTGAAAGACATGACACTGACGACAAACAATGAAAGAAAGA 139
DB 112 TGACACTCTGTGCGCAATATTGAAAGACATGACACTGACGACAAACAATGAAAGAAAGA 171
OY 140 TAAAGTCGGTATTGAAAGACATGAGACACATGTAAGTGAATAAGTAAAGGC 199
DB 172 TAAAGTCGGTATTG- AAGACATGAGACACATGTAAGTGAATAAGTAAAGGC 230
OY 200 GGAAGTAACCTTATGCACTTTGTAATTGGTTAC 233
DB 231 GGAAGTAACCTTATGCACTTTGTAATTGGTTAC 264
RESULT 10
AAA96839
ID AAA96839 standard; DNA; 371 BP.
XX
```

AC	AAA96839;
XX	
DT	19-FEB-2001 (first entry)
XX	
DE	Nucleotide sequence of chimeric expression promoter MPR1146.
XX	
KW	Promoter; intergenic region; Commelina yellow mottle virus;
KV	chimeric expression promoter; plant vascular expression promoter;
KW	plant green tissue expression promoter; Cassava vein mosaic virus;
XX	transgenic plant; chimera; ss.
OS	
OS	Chimeric - Commelina yellow mottle virus.
OS	Chimeric - Cassava vein mosaic virus.
PN	
PN	WO200058485-A1.
PD	
PD	05-OCT-2000.
XX	
PE	29-MAR-2000; 2000WO-IB00370.
XX	
PR	29-MAR-1999; 99FR-0003925.
XX	
PA	(MERI-) MERISTEM THERAPEUTICS.
XX	
PI	Rance I, Gruber V, Theisen M;
DR	WPI; 2000-647238/62.
PT	
PT	Chimeric expression promoter for transgenic plant production, comprises
PT	sequence from promoter comprising vascular expression region replaced
PT	with sequence from promoter comprising green tissue expression region
PS	-
XX	
PS	Claim 5; Page 81; 91pp; English.
XX	
CC	The present sequence represents a chimeric promoter of the invention.
CC	The specification describes chimeric expression promoters. These
CC	chimeric promoters comprise a nucleic acid sequence which is derived
CC	from a first plant promoter, in which a plant vascular expression
CC	promoter region is replaced with a nucleic acid sequence derived from
CC	a second plant promoter comprising a plant green tissue expression
CC	promoter region. Preferably, the first plant promoter originates from
CC	Commelina yellow mottle virus, and the second plant promoter originates
CC	from the Cassava vein mosaic virus. Especially, the promoters are
CC	derived from intergenic regions. The chimeric promoters are useful
CC	for producing transgenic plants.
XX	
SQ	Sequence 371 BP; 122 A; 68 C; 89 G; 92 T; 0 other;
	Query Match 33.1%; Score 152.8; DB 21; Length 371;
	Best Local Similarity 98.7%; Pred. No. 7.1e-37;
	Matches 154; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	78 CATGCATCTGTCGGCATATTGAAGACGTAAAGCACTGACGCCAACAATGAAAGAAGAA 137
DB	130 CATGCCACTCTGTGGCAATATTGAAGACGTAAAGCACTGACGCCAACAATGAAAGAAGAA 189
OY	138 GATAAGTCCGCGATTTGGAAGAAGACATATGAGGACACATGTAAGTGGAATGTAAAGC 197
DB	190 GATTAAGTCCGCGATTTGGAAGAAGACATATGAGGACACATGTAAGTGGAATGTAAAGC 249
OY	198 GCGAAGTAACCTTATGCATTTGTAAATTTGGTTAC 233
DB	250 GCGAAGTAACCTTATGCATTTGTAAATTTGGTTAC 285
	RESULT 11
ID	AAA96841
AC	AAA96841 standard; DNA; 301 BP.
XX	
AC	AAA96841;
XX	
PT	19-FEB-2001 (first entry)

XX	Nucleotide sequence of chimeric expression promoter MP1154.	
XX		
XX	Promoter; intergenic region; Commelina yellow mottle virus;	
KV	chimeric expression promoter; plant vascular expression promoter;	
KW	plant green tissue expression promoter; Cassava vein mosaic virus;	
KX	transgenic plant; chimera; ss.	
XX		
OS	Chimeric - Commelina yellow mottle virus.	
OS	Chimeric - Cassava vein mosaic virus.	
XX		
PN	WO200058485-A1.	
PD		
PD	05-OCT-2000.	
PF	29-MAR-2000; 2000WO-IB00370.	
XX		
PR	29-MAR-1999; 99FR-0003925.	
XX		
PA	(MERI-) MERISTEM THERAPEUTICS.	
PI		
PI	Rance I, Gruber V, Theisen M;	
XX		
DR	WPI: 2000-647238/62.	
XX		
PT	Chimeric expression promoter for transgenic plant production, comprises	
PT	sequence from promoter comprising vascular expression region replaced	
PT	with sequence from promoter comprising green tissue expression region	
XX		
PS	Claim 5; Page 82; 91pp; English.	
XX		
CC	The present sequence represents a chimeric promoter of the invention.	
CC	The specification describes chimeric expression promoters. These	
CC	chimeric promoters comprise a nucleic acid sequence which is derived	
CC	from a first plant promoter, in which a plant vascular expression	
CC	promoter region is replaced with a nucleic acid sequence derived from	
CC	a second plant promoter comprising a plant green tissue expression	
CC	promoter region. Preferably, the first plant promoter originates from	
CC	Commelina yellow mottle virus, and the second plant promoter originates	
CC	from the Cassava vein mosaic virus. Especially, the promoters are	
CC	derived from intergenic regions. The chimeric promoters are useful	
CC	for producing transgenic plants.	
XX		
SO	Sequence 301 BP; 98 A; 54 C; 74 G; 75 T; 0 other;	
XX		
Query Match	30.5%; Score 140.8; DB 21; Length 301;	
	Best Local Similarity 98.1%; Pred. No. 3.1e-33;	
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;		
QY	78 CATGCACTCTGTGGGATATTGAAGAGTAAGCACTGACGACCAACATGAAAGAGA 137	
DB	63 CATGCCACTCTGTGGGATATTGAAGAGTAAGCACTGACGACCAACATGAAAGAGA 122	
QY	138 GATAAGTCTGGTGAATTGTGAAGAGACATAGACACATGTAAGGTGAAATGTAAAG 197	
DB	123 GATAAGTCTGGTGAATTGTG - AAGAGACATAGAGACACATGTAAGGTGAAATGTAAAG 181	
QY	198 GCGGAAGTAACCTTATGCAATTTGTAATTTGGTTAC 233	
DB	182 GCGGAAGTAACCTTATGCAATTTGTAATTTGGTTAC 217	
XX		
RESULT 12		
AAID	AAA96840	
AC	AAA96840 standard; DNA; 398 BP.	
AC	AAA96840;	
XX		
DT	19-FEB-2001 (first entry)	
XX		
DE	Nucleotide sequence of chimeric expression promoter MP1147.	
XX		

KM Promoter; intergenic region; Commelina yellow mottle virus;
 KM chimeric expression promoter; plant vascular expression promoter;
 KM plant green tissue expression promoter; Cassava vein mosaic virus;
 KM transgenic plant; chimera; ss.
 OS Chimeric - Commelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.
 PN WO200058485-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 29-MAR-2000; 2000WO-IB00370.
 XX
 PR 29-MAR-1999; 99PR-0003925.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX
 DR WPI; 2000-647238/62.
 XX
 PT Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region
 PT -
 XX
 PS Claim 5; Page 82; 91pp; English.
 XX
 CC The present sequence represents a chimeric promoter of the invention.
 CC The specification describes a chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Commelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 XX
 SO Sequence 398 BP; 128 A; 80 C; 93 G; 97 T; 0 other;
 XX
 Query Match 30.5%; Score 140.8; DB 21; Length 398;
 Best Local Similarity 98.1%; Pred. No. 3.5e-33;
 Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 XX
 QY 78 CATGACACTGTGGCAATTTGAAGCCTAAGCAGTGAAGACACATATAAAGAA 137
 DB 160 CATGCCACTGTGGCAATTTGAAGCAGTGAAGCAGCAGCAATGAAAAAGAA 219
 QY 138 GATAAGTCGCTGATTGTGAAGAGACATAGAGACATGTAAGTGAATGTAAG 197
 DB 220 GATAAGTCGCTGATTGTG-AAGAGACATAGAGACACATGTAAGTGAAGT 278
 QY 198 GCGGAAAGTAACCTTATGCAATTTGTAATTTGGTTAC 233
 DB 279 GCGGAAAGTAACCTTATGCAATTTGTAATTTGGTTAC 314
 XX
 RESULT 13
 ID AAV14019 standard; DNA; 392 BP.
 XX
 AC AAV14019;
 XX
 DT 18-JUN-1998 (first entry)
 XX
 DE CSMVW promoter CVP1.
 XX
 KM Cassava vein mosaic virus; CSMVW; promoter; cultivated crop;
 KM tissue-specific expression control; transgenic plant; ss.
 XX

OS Cassava vein mosaic virus.
 XX
 PN WO9748819-A1.
 XX
 PD 24-DEC-1997.
 XX
 PF 20-JUN-1997; 97WO-US10376.
 XX
 PR 20-JUN-1996; 96US-0020129.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Beachy RN, De Kochko A, Fauquet C, Verdaguer B;
 XX
 DR WPI; 1998-063157/06.
 XX
 PT Cassava vein mosaic virus promoter - used to express heterologous
 PT DNA sequences for producing transgenic plants having altered
 PT phenotype(s)
 XX
 PS Claim 2; Page 74; 115pp; English.
 XX
 CC This sequence represents a cassava vein mosaic virus promoter, and
 CC is a nucleic acid molecule of the invention. The promoter is capable of
 CC initiating transcription of an operably linked heterologous nucleic acid
 CC sequence in a plant cell. The CSMVW promoters are active in both monocot
 CC and dicot plant species, and therefore can be readily applied to a
 CC variety of cultivated crops. Although generally constitutive, the
 CC derivative promoters include promoters that can regulate expression in a
 CC tissue-specific manner, and therefore are useful for controlling
 CC expression of heterologous genes in a tissue-specific manner. The
 CC promoters can be used for producing transgenic plants with an altered
 CC phenotype.
 XX
 SO Sequence 392 BP; 154 A; 64 C; 83 G; 91 T; 0 other;
 XX
 Query Match 26.1%; Score 120.6; DB 19; Length 392;
 Best Local Similarity 93.3%; Pred. No. 5.5e-27;
 Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 XX
 QY 93 GAATATTGAAGAGCTAAGCCTGAGCAACATGAAAGAGATTAAGTCGCTGAT 152
 DB 143 GAATCTTGAAGAGCTAAGCCTGAGCAACATGAAAGAGATTAAGTCGCTGAT 202
 QY 153 TGTGAAGAGACATAGAGACATGTAAGTGAATGTGAAGCGGAAAGTAACTTT 212
 DB 203 TGTGAAGAGACATAGAGAGACATGTAAGTGAATGTGAAGCGGAAAGTAACTTT 262
 QY 213 ATGCATTTGTAATTT 227
 DB 263 ATCAACAAGCAATCT 277
 XX
 RESULT 14
 ID AAV14021 standard; DNA; 411 BP.
 XX
 AC AAV14021;
 XX
 DT 18-JUN-1998 (first entry)
 XX
 DE CSMVW promoter PB.
 XX
 KM Cassava vein mosaic virus; CSMVW; promoter; cultivated crop;
 KM tissue-specific expression control; transgenic plant; ss.
 XX
 OS Cassava vein mosaic virus.
 XX
 PN WO9748819-A1.
 XX
 PD 24-DEC-1997.
 XX
 PF 20-JUN-1997; 97WO-US10376.
 XX

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XX 20-JUN-1996; 96US-0020129.
PR (SCRI ) SCRIPPS RES INST.
PA Beachy RN, De Kochko A, Fauquet C, Verdagner B;
XX WPI; 1998-063157/06.
DR
XX
XX Cassava vein mosaic virus promoter - used to express heterologous
PT DNA sequences for producing transgenic plants having altered
PT phenotype(s)
XX
XX Claim 2; Page 76-77; 115pp; English.
XX
XX This sequence represents a cassava vein mosaic virus promoter, and
CC is a nucleic acid molecule of the invention. The promoter is capable of
CC initiating transcription of an operably linked heterologous nucleic acid
CC sequence in a plant cell. The CaMV promoters are active in both monocot
CC and dicot plant species, and therefore can be readily applied to a
CC variety of cultivated crops. Although generally constitutive, the
CC derivative promoters include promoters that can regulate expression in a
CC tissue-specific manner, and therefore are useful for controlling
CC expression of heterologous genes in a tissue-specific manner. The
CC promoters can be used for producing transgenic plants with an altered
CC phenotype.
XX
SQ Sequence 411 BP; 157 A; 60 C; 87 G; 107 T; 0 other;

Query Match 26.1%; Score 120.6; DB 19; Length 411;
Best Local Similarity 93.3%; Pred. No. 5.6e-27;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGACCTAAGCACTGACGACACATGAAAAGAAAGATAGGTGGTGAT 152
DB 107 GAACTCTGAAGACCTAAGCACTGACGACACATGAAAAGAAAGATAGGTGGTGAT 166
QY 153 TGTGAAAGAGACATAGAGACACATGTAAGTGGAAAATGTAAGCGCGAAAGTAACCTT 212
DB 167 TGTGAAAGAGACATAGAGACACATGTAAGTGGAAAATGTAAGCGCGAAAGTAACCTT 226
QY 213 ATGCATTTGTAATTT 227
DB 227 ATCACAAAGCAATCT 241

RESULT 15
AAA96836
ID AAA96836 standard; DNA; 515 BP.
XX
XX AAA96836;
AC
XX
XX 19-FEB-2001 (first entry)
DT
XX
XX Promoter from intergenic region of Cassava vein mosaic virus.
DE
XX
XX Promoter; intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
transgenic plant; ss.
XX
XX Cassava vein mosaic virus.
OS
XX
XX MO200058485-A1.
PN
XX
XX 05-OCT-2000.
PD
XX
XX 29-MAR-2000; 2000MO-IB00370.
PF
XX
XX 29-MAR-1999; 99FR-0003925.
PR
XX
XX (MERI-) MERISTEM THERAPEUTICS.
PA
XX
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```
PI Rance I, Gruber V, Thelsen M;
XX
XX WPI; 2000-647238/62.
DR
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 4; Page 80; 91pp; English.
XX
XX The present sequence represents a promoter fragment from the intergenic
CC region of Cassava vein mosaic virus. The promoter is used to construct
CC chimeric expression promoters. These chimeric promoters comprise a
CC nucleic acid sequence which is derived from a first plant promoter,
CC in which a plant vascular expression promoter region is replaced with
CC a nucleic acid sequence derived from a second plant promoter comprising
CC a plant green tissue expression promoter region. Preferably, the first
CC plant promoter originates from Commelina yellow mottle virus, and the
CC second plant promoter originates from the Cassava vein mosaic virus.
CC The chimeric promoters are useful for producing transgenic plants.
XX
XX
SQ Sequence 515 BP; 198 A; 79 C; 109 G; 129 T; 0 other;

Query Match 26.1%; Score 120.6; DB 21; Length 515;
Best Local Similarity 93.3%; Pred. No. 6.1e-27;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGACCTAAGCACTGACGACACATGAAAAGAAAGATAGGTGGTGAT 152
DB 216 GAACTCTGAAGACCTAAGCACTGACGACACATGAAAAGAAAGATAGGTGGTGAT 275
QY 153 TGTGAAAGAGACATAGAGACACATGTAAGTGGAAAATGTAAGCGCGAAAGTAACCTT 212
DB 276 TGTGAAAGAGACATAGAGACACATGTAAGTGGAAAATGTAAGCGCGAAAGTAACCTT 335
QY 213 ATGCATTTGTAATTT 227
DB 336 ATCACAAAGCAATCT 350
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Search completed: April 14, 2003, 08:19:38
Job time : 151.237 secs

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:01:47 ; Search time 47.6289 Seconds
(without alignments)
2974.765 Million cell updates/sec

Title: US-09-963-803-20

Perfect score: 462

Sequence: 1 aagcttcacatgcctgcagca.....cacacaactagagatcc 462

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/lna/PCRUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/lna/backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48.6	10.5	7218	1	Sequence 14, Appl
2	40.4	8.7	439	1	Sequence 3, Appl
3	40.4	8.7	439	2	Sequence 3, Appl
4	40.4	8.7	446	1	Sequence 23, Appl
5	40.4	8.7	532	3	Sequence 1, Appl
6	40.4	8.7	532	4	Sequence 1, Appl
7	40.4	8.7	532	4	Sequence 1, Appl
8	40.4	8.7	532	4	Sequence 1, Appl
9	40.4	8.7	532	4	Sequence 1, Appl
10	40.4	8.7	532	4	Sequence 1, Appl
11	40.4	8.7	532	4	Sequence 1, Appl
12	40.4	8.7	532	4	Sequence 1, Appl
13	40.4	8.7	560	3	Sequence 5, Appl
14	40.4	8.7	560	4	Sequence 5, Appl
15	40.4	8.7	560	4	Sequence 5, Appl
16	40.4	8.7	560	4	Sequence 5, Appl
17	40.4	8.7	560	4	Sequence 5, Appl
18	40.4	8.7	560	4	Sequence 5, Appl
19	40.4	8.7	560	4	Sequence 5, Appl
20	40.4	8.7	560	4	Sequence 5, Appl
21	40.4	8.7	661	4	Sequence 33, Appl
22	40.4	8.7	793	4	Sequence 1, Appl
23	40.4	8.7	793	4	Sequence 1, Appl
24	40.4	8.7	831	1	Sequence 5, Appl
25	40.4	8.7	950	6	Patent No. 5177308
26	40.4	8.7	978	1	Sequence 31, Appl
27	40.4	8.7	978	1	Sequence 31, Appl

28	40.4	8.7	979	1	US-08-446-486-30	Sequence 30, Appl
29	40.4	8.7	979	1	US-08-463-308-30	Sequence 30, Appl
30	40.4	8.7	980	6	5254799-30	Patent No. 5254799
31	40.4	8.7	1030	1	US-07-936-163-46	Sequence 46, Appl
32	40.4	8.7	1030	4	US-08-729-601A-43	Sequence 43, Appl
33	40.4	8.7	1034	4	US-09-363-970-35	Sequence 35, Appl
34	40.4	8.7	1138	4	US-09-011-151-8	Sequence 8, Appl
35	40.4	8.7	1138	4	US-09-011-151-9	Sequence 9, Appl
36	40.4	8.7	1196	4	US-08-729-601A-46	Sequence 46, Appl
37	40.4	8.7	1279	4	US-09-185-244-2	Sequence 2, Appl
38	40.4	8.7	1279	4	US-09-471-913-6	Sequence 6, Appl
39	40.4	8.7	1303	3	US-08-894-440-2	Sequence 2, Appl
40	40.4	8.7	1303	4	US-09-458-093-2	Sequence 2, Appl
41	40.4	8.7	1651	3	US-09-065-999-5	Sequence 5, Appl
42	40.4	8.7	1651	3	US-09-065-999-6	Sequence 6, Appl
43	40.4	8.7	1722	1	US-08-247-809A-5	Sequence 5, Appl
44	40.4	8.7	1722	2	US-08-711-728-5	Sequence 5, Appl
45	40.4	8.7	1829	1	US-07-966-187-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHIEFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOXLX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pc-F1s
US-08-232-463-14
Query Match 10.5% Score 48.6; DB 1; Length 7218;

Best Local Similarity 5.38; Pred. No. 2.7e-05;
Matches 18; Conservative 185; Mismatches 134; Indels 0; Gaps 0;

OY 59 GAGAGATGATAGCTGACCTGACACTCTGTGGCAATATTGGAAGAGCTAGCAGC 118
DB 1367 RRR 1308
OY 119 ACAACAATGAAAGAGAGATAAGTCGGTGAATTGTGAAGACATAGAGACATG 178
DB 1307 RRR 1248
OY 179 TAAGTGAAGAAATGTAAGCGCGAAGTAACCTTATGCAATTTGATTGTTACGACTA 238
DB 1247 RRR 1188
OY 239 GTGATGATGATATCAAGATGATGATATCTCCACTGACGTAAGGATGACGATG 298
DB 1187 RRR 1128
OY 299 CCAGACTAGTATGATGATGATATCAAGATGATGATGATGATGATGATGATGATG 358
DB 1127 RRR 1068
OY 359 TGACGATGCCAGCTTACCGGATATGCCGTTCCCA 395
DB 1067 RATCGAAGCTCCCTCGACTGACGCAAGCTCGAA 1031

RESULT 2

US-08-247-809A-3
; Sequence 3, Application US/08247809A
; Patent No. 5569823
; GENERAL INFORMATION:
; APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;
; APPLICANT: Edgar Maiss
; TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
; MEDIUM TYPE: storage
; COMPUTER: NEC Powermate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/247,809A
; FILING DATE: May 23, 1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 43 178 45.6 (Germany)
; FILING DATE: May 28, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 9049-KGB.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-247-809A-3

Query Match 8.7%; Score 40.4; DB 1; Length 439;
Best Local Similarity 88.0%; Pred. No. 0.0028;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACGACTA 307
DB 338 GATTGATGATATCTCCACTGACGTAAAGGATGACGACCAATCCGACTA 387

RESULT 3

US-08-711-728-3
; Sequence 3, Application US/08711728
; Patent No. 5973135
; GENERAL INFORMATION:
; APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;
; APPLICANT: Edgar Maiss
; TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
; MEDIUM TYPE: storage
; COMPUTER: NEC Powermate 1 Plus
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,728
; FILING DATE: 03-SEPT-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/247,809
; FILING DATE: 23-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 43178456
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 9049.1-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-711-728-3

Query Match 8.7%; Score 40.4; DB 2; Length 439;
Best Local Similarity 88.0%; Pred. No. 0.0028;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACGACTA 307
DB 338 GATTGATGATATCTCCACTGACGTAAAGGATGACGACCAATCCGACTA 387

RESULT 4
US-08-764-100-23
; Sequence 23, Application US/08764100
; Patent No. 5773700
; GENERAL INFORMATION:


```

: APPLICANT: van Gilsven J., Martinus O.
: APPLICANT: De Haan, Petrus T.
: APPLICANT: Giejen L., Johannes J.
: APPLICANT: Peters, Dirk
: APPLICANT: Goldbach, Robert W.
: TITLE OF INVENTION: Improvements in or Relating to Organic
: TITLE OF INVENTION: Compounds
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sandoz Agro, Inc
: STREET: 975 California Avenue
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/764,100
: FILING DATE: 06-DEC-1996
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/214,064
: FILING DATE:
: APPLICATION NUMBER: US 08/032,235
: FILING DATE: 17-MAR-1993
: APPLICATION NUMBER: GB 9206016.9
: FILING DATE: 19-MAR-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: NO. 5773700rls, Allen E.
: REGISTRATION NUMBER: 34,490
: REFERENCE/DOCKET NUMBER: 137-1061
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 354-3592
: TELEFAX: (415) 857-1125
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 446 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-08-764-100-23
:
: Query Match      8.7%; Score 40.4; DB 1; Length 446;
: Best Local Similarity 88.0%; Pred. No. 0.0028;
: Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
:
: Oy      258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACGACTA 307
: Db      274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 323
:
: RESULT 5
: US-09-042-426-1
: Sequence 1, Application US/09042426
: Patent No. 6114608
: GENERAL INFORMATION:
: APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
: TITLE OF INVENTION: DNA Construct Containing Bacillus
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NO. 6114608artls Corporation
: STREET: 564 Morris Avenue
: CITY: Summit
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07901
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/291,238
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/042,426
: FILING DATE: March 13, 1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoxie, Thomas
: REGISTRATION NUMBER: 32,993
: REFERENCE/DOCKET NUMBER: 135/1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8614
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 532 base pairs
: TYPE: nucleic acid
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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/042,426
: FILING DATE: March 13, 1998
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoxie, Thomas
: REGISTRATION NUMBER: 32,993
: REFERENCE/DOCKET NUMBER: 135/1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8614
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 532 base pairs
: TYPE: nucleic acid
:
: US-09-042-426-1
:
: Query Match      8.7%; Score 40.4; DB 3; Length 532;
: Best Local Similarity 88.0%; Pred. No. 0.003;
: Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
:
: Oy      258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACGACTA 307
: Db      274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 323
:
: RESULT 6
: US-09-291-238-1
: Sequence 1, Application US/09291238
: Patent No. 622104
: GENERAL INFORMATION:
: APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
: TITLE OF INVENTION: DNA Construct Containing Bacillus
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NO. 622104artls Corporation
: STREET: 564 Morris Avenue
: CITY: Summit
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07901
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/291,238
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/042,426
: FILING DATE: March 13, 1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoxie, Thomas
: REGISTRATION NUMBER: 32,993
: REFERENCE/DOCKET NUMBER: 135/1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8614
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 532 base pairs
: TYPE: nucleic acid
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-291-238-1

Query Match 8.7% Score 40.4; DB 4; Length 532;
Best Local Similarity 88.0%; Pred. No. 0.003;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 307
DB 274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGACCAATCCACTA 323

RESULT 7

US-09-330-760-1
Sequence 1, Application US/09330760
Patent No. 6229075
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Stinbald
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6229075artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-330-760-1

Query Match 8.7% Score 40.4; DB 4; Length 532;
Best Local Similarity 88.0%; Pred. No. 0.003;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 307
DB 274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGACCAATCCACTA 323

RESULT 8
US-09-328-473-1
Sequence 1, Application US/09328473
Patent No. 6232533

GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Stinbald
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6232533artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,473
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-328-473-1

Query Match 8.7% Score 40.4; DB 4; Length 532;
Best Local Similarity 88.0%; Pred. No. 0.003;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 307
DB 274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGACCAATCCACTA 323

RESULT 9

US-09-330-737-1
Sequence 1, Application US/09330737
Patent No. 6232534
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Stinbald
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6232534artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,737
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-330-737-1

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 4; Length 532;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 307
|||||
DB 274 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 323

RESULT 10
US-09-329-169-1
Sequence 1, Application US/09329169
Patent No. 6329575
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6329575artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,169
FILING DATE: 09-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614

TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-329-169-1

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 4; Length 532;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 307
|||||
DB 274 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 323

RESULT 11
US-09-330-714A-1
Sequence 1, Application US/09330714A
Patent No. 6342660
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6342660artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,714A
FILING DATE: 11-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-330-714A-1

Query Match 8.7%; Score 40.4; DB 4; Length 532;
Best Local Similarity 88.0%; Pred. No. 0.003;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTGACGTAGGATGACGATGCCAGCTA 307
|||||
Db 274 GATTGATGTGATATCTCCAGCTGACGTAGGATGACGATGCCAGCTA 323
|||||

RESULT 12
US-09-328-826-1
Sequence 1, Application US/09328826
Patent No. 6399860
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6399860artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,826
FILING DATE: 09-Jun-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-328-826-1

Query Match 8.7%; Score 40.4; DB 4; Length 532;
Best Local Similarity 88.0%; Pred. No. 0.003;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTGACGTAGGATGACGATGCCAGCTA 307
|||||
Db 274 GATTGATGTGATATCTCCAGCTGACGTAGGATGACGATGCCAGCTA 323
|||||

RESULT 13
US-09-042-426-5
Sequence 5, Application US/09042426
Patent No. 6114608
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6114608artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-042-426-5

Query Match 8.7%; Score 40.4; DB 3; Length 560;
Best Local Similarity 88.0%; Pred. No. 0.0031;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTGACGTAGGATGACGATGCCAGCTA 307
|||||
Db 322 GATTGATGTGATATCTCCAGCTGACGTAGGATGACGATGCCAGCTA 371
|||||

RESULT 14
US-09-291-238-5
Sequence 5, Application US/09291238
Patent No. 6222104
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6222104artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998

ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-291-238-5

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 4; Length 560;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 258 GATTGATGTGATATCTCCACTGACGCTAAGGATGACGATGCCAGACTA 307
|||||
Db 322 GATTGATGTGATATCTCCACTGACGCTAAGGATGACGACATCCCACTA 371

RESULT 15
US-09-330-760-5
Sequence 5, Application US/09330760
Patent No. 6229075
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6229075artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:

CLONE: 35S Promoter
US-09-330-760-5

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 4; Length 560;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 258 GATTGATGTGATATCTCCACTGACGCTAAGGATGACGATGCCAGACTA 307
|||||
Db 322 GATTGATGTGATATCTCCACTGACGCTAAGGATGACGACATCCCACTA 371

Search completed: April 14, 2003, 10:28:36
Job time : 53.6289 secs

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:29:46 ; Search time 55.567 Seconds
(without alignments)
7293.024 Million cell updates/sec

Title: US-09-963-803-20

Perfect score: 462

Sequence: 1 aaagctgcatgcctgcagca.....cacacaacctaagagatcc 462

Scoring table: IDENTITY_NUC

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published_Applications_NA.*
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3: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	100.0	462	US-09-963-803-20	Sequence 20, Appl
2	373.6	80.9	600	US-09-963-803-22	Sequence 22, Appl
3	354.2	76.7	541	US-09-963-803-24	Sequence 24, Appl
4	314	68.0	393	US-09-963-803-19	Sequence 19, Appl
5	262	56.7	604	US-09-963-803-23	Sequence 23, Appl
6	240.2	52.0	317	US-09-963-803-21	Sequence 21, Appl
7	212.4	46.0	317	US-09-963-803-3	Sequence 3, Appl
8	212.4	46.0	472	US-09-963-803-25	Sequence 25, Appl
9	200.4	43.4	348	US-09-963-803-4	Sequence 4, Appl
10	152.8	33.1	371	US-09-963-803-5	Sequence 5, Appl
11	140.8	30.5	301	US-09-963-803-7	Sequence 7, Appl
12	140.8	30.5	398	US-09-963-803-6	Sequence 6, Appl
13	120.6	26.1	515	US-09-963-803-2	Sequence 2, Appl
14	120.6	26.1	532	US-09-765-555-1	Sequence 1, Appl
15	120.6	26.1	8340	US-09-847-057-4	Sequence 4, Appl
16	120.6	26.1	8340	US-09-874-926-4	Sequence 4, Appl
17	120.6	26.1	12241	US-10-033-190-5	Sequence 5, Appl
18	80	17.3	243	US-09-963-803-1	Sequence 1, Appl
19	75.4	16.3	392	US-09-963-803-21	Sequence 21, Appl

20	69.6	15.1	79	9	US-09-963-803-14	Sequence 14, Appl
21	62	13.4	62	9	US-09-963-803-10	Sequence 10, Appl
22	60	13.0	60	9	US-09-963-803-9	Sequence 9, Appl
23	60	13.0	63	9	US-09-963-803-12	Sequence 12, Appl
24	58	12.6	80	10	US-09-870-375-34	Sequence 34, Appl
25	58	12.6	236	10	US-09-870-375-35	Sequence 35, Appl
26	58	12.6	299	10	US-09-870-375-36	Sequence 36, Appl
27	58	12.6	332	10	US-09-870-375-7	Sequence 7, Appl
28	58	12.6	472	10	US-09-870-375-5	Sequence 5, Appl
29	55	11.9	65	9	US-09-963-803-8	Sequence 8, Appl
30	55	11.9	80	10	US-09-870-375-28	Sequence 28, Appl
31	45	9.7	63	9	US-09-963-803-13	Sequence 13, Appl
32	41.6	9.0	671	9	US-10-184-644-346	Sequence 346, Appl
33	40.4	8.7	566	10	US-09-943-692-33	Sequence 33, Appl
34	40.4	8.7	661	10	US-09-943-692-33	Sequence 33, Appl
35	40.4	8.7	700	9	US-10-138-221-9	Sequence 9, Appl
36	40.4	8.7	763	9	US-10-162-214-9	Sequence 9, Appl
37	40.4	8.7	3983	9	US-09-758-987-1	Sequence 1, Appl
38	40.4	8.7	4973	9	US-09-990-659A-15	Sequence 15, Appl
39	40.4	8.7	5767	9	US-09-810-861B-3	Sequence 3, Appl
40	40.4	8.7	7129	9	US-10-047-543-101	Sequence 10, Appl
41	40.4	8.7	13737	9	US-10-074-279-10	Sequence 4, Appl
42	40.4	8.7	14446	9	US-09-810-861B-4	Sequence 33, Appl
43	39.2	8.5	63	10	US-09-870-375-33	Sequence 8, Appl
44	39.2	8.5	219	10	US-09-870-375-8	Sequence 9, Appl
45	39.2	8.5	282	10	US-09-870-375-9	

ALIGNMENTS

RESULT 1

US-09-963-803-20
Sequence 20, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 462
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MPr1163
NAME/KEY: promoter
LOCATION: (1)..(462)
OTHER INFORMATION:
US-09-963-803-20

Query Match 100.0%; Score 462; DB 9; Length 462;

Best Local Similarity 100.0%; Pred. No. 5.8e-129; Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCTGATGCTGCGAGCACTAGTATCCGCGCTCATCATGACATGACAGTACTGA 60
DB 1 AACCTGATGCTGCGAGCACTAGTATCCGCGCTCATCATGACATGACAGTACTGA 60
QY 61 GGAGATGAATAGTACCATGACACTCTGTGCGAATATTTGAAGACGTAAGCACTGACGAC 120
DB 61 GGAGATGAATAGTACCATGACACTCTGTGCGAATATTTGAAGACGTAAGCACTGACGAC 120
QY 121 AACATGAAAAGAGAAGATTAAGTTCGATTTGTGAAGAGACATTAAGAGACATGTA 180

Db 121 AACATGAAAAGAGATAAGTGGGATGTGAAAGACATAGAGACACATGTA 180
Qy 181 AGGTGAAAATGCTAAGGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGT 240
Db 181 AGGTGAAAATGCTAAGGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGT 240
Qy 241 GATTGATGTGATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 300
Db 241 GATTGATGTGATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 300
Qy 301 ACGACTAGTGTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG 360
Db 301 ACGACTAGTGTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG 360
Qy 361 ACGCATGCCAGCTTACCCGGTATGCCGGTCCCAAGCTTTATTTCTTATTTAAGCACTT 420
Db 361 ACGCATGCCAGCTTACCCGGTATGCCGGTCCCAAGCTTTATTTCTTATTTAAGCACTT 420
Qy 421 GTGTAGTACCTAGAAAACCAACACACACACCTAGAGATCC 462
Db 421 GTGTAGTACCTAGAAAACCAACACACACACCTAGAGATCC 462

RESULT 2

US-09-963-803-22
: Sequence 22, Application US/09963803
: Publication No. US20030028922A1
: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow n
: FILE REFERENCE: 184332042
: CURRENT FILING DATE: 2001-09-26
: PRIOR FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: FR 99/03925
: PRIOR FILING DATE: 2000-10-05
: PRIOR APPLICATION NUMBER: PCT IB00/00370
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 22
: LENGTH: 600
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: promoter MP-1165
: NAME/KEY: promoter
: LOCATION: (1)..(600)
: OTHER INFORMATION:
US-09-963-803-22

Query Match 80.9%: Score 373.6; DB 9; Length 600;

Best Local Similarity 95.3%: Pred. No. 2.2e-102; Matches 383; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 AAGCTTGATGCTGCACACACTAGTATCCGCCATCATCAATGACATCATCAGACTGCA 60
Db 1 AAGCTTGATGCTGCACACACTAGTATCCGCCATCATCAATGACATCATCAGACTGCA 60
Qy 61 GGAGTGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCACTAGCAG 120
Db 61 GGAGTGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCACTAGCAG 120
Qy 121 AACATGAAAAGAGATAAGTGGGATGTGAAAGACATAGAGACACATGTA 180
Db 121 AACATGAAAAGAGATAAGTGGGATGTGAAAGACATAGAGACACATGTA 180
Qy 181 AGGTGAAAATGCTAAGGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGT 240
Db 181 AGGTGAAAATGCTAAGGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGT 240

Qy 241 GATTGATGTGATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 300
Db 241 GATTGATGTGATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 300
Qy 301 ACGACTAGTGTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG 360
Db 301 ACGACTAGTGTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG 360
Qy 361 ACGCATGCCAGCTTACCCGGTATGCCGGTCCCAAGCTTTATTTCTTATTTAAGCACTT 404
Db 361 ACGCATGCCAGCTTACCCGGTATGCCGGTCCCAAGCTTTATTTCTTATTTAAGCACTT 404

RESULT 3

US-09-963-803-24
: Sequence 24, Application US/09963803
: Publication No. US20030028922A1
: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
: FILE REFERENCE: 184332042
: CURRENT FILING DATE: 2001-09-26
: PRIOR FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: FR 99/03925
: PRIOR FILING DATE: 2000-10-05
: PRIOR APPLICATION NUMBER: PCT IB00/00370
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 24
: LENGTH: 541
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: promoter MP-1168
: NAME/KEY: promoter
: LOCATION: (1)..(541)
: OTHER INFORMATION:
US-09-963-803-24

Query Match 76.7%: Score 354.2; DB 9; Length 541;

Best Local Similarity 98.4%: Pred. No. 1.4e-96; Matches 379; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

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Db 160 CATGACACCTGTCGGATATTGAAGAGCTAGACCTGACGCAACATGAAAAGAGAA 219
Qy 138 GATAAGTCTGGTATTGTAAGAGACATAGAGACACATGTAAGTGGAATGTAAG 197
Db 220 GATAAGTCTGGTATTGTAAGAGACATAGAGACACATGTAAGTGGAATGTAAG 278
Qy 198 GCGGAAAGTAACTTATGCAATTTGGTTACGACTGATGATTTATGATATGTA 257
Db 279 GCGGAAAGTAACTTATGCAATTTGGTTACGACTGATGATTTATGATATGTA 338
Qy 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCAAGCTAGATTGATG 317
Db 339 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCAAGCTAGATTGATG 398
Qy 318 TGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCAAGCT 377
Db 399 TGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCAAGCT 458
Qy 378 CGGTATGCCGGTCCCAAGCTTTATTTCTTATTTAAGCACTTGTGTAGCTTAGAA 437
Db 459 CGGTATGCCGGTCCCAAGCTTTATTTCTTATTTAAGCACTTGTGTAGCTTAGAA 516
Qy 438 ACCAACACACACCTAGAGATCC 462
Db 517 ACCAACACACACCTAGAGATCC 541


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Db 123 GATTAAGGTCGGTATTGTG-AAGGACATAGAGACACATGAAGTGGAATGTAAAG 181
QY 198 GCGGAAGTAACCTTATGCAATTTGTAATTTGGTTAC 233
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RESULT 12
US-09-963-803-6
; Sequence 6, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: promoter MPr1147
; LOCATION: (1)..(398)
; OTHER INFORMATION:
US-09-963-803-6

Query Match 30.5%; Score 140.8; DB 9; Length 398;
Best Local Similarity 98.1%; Pred. No. 1.4e-32;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db 160 CATGCCACTGTGCGCAATTTGGAAGCGTAAGCAGTACGACACATGTAAGAAAGAA 219
QY 138 GATAAGTCGGTATTGTGAAGAGACATAGAGACATGTAAGTGGAATTTGTAAGG 197
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Db 220 GATAAGTCGGTATTGTG-AAGAGACATAGAGACACATGTAAGTGGAATTTGTAAGG 278
QY 198 GCGGAAGTAACCTTATGCAATTTGTAATTTGGTTAC 233
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Db 279 GCGGAAGTAACCTTATGCAATTTGTAATTTGGTTAC 314

RESULT 13
US-09-963-803-2
; Sequence 2, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 515
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from the intergenic region of Cassava Vein Mosaic v1
; OTHER INFORMATION: of 515 bp in length EMBL
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(515)
; OTHER INFORMATION:
US-09-963-803-2

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Best Local Similarity 93.3%; Pred. No. 1.8e-26;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGAGCTAAGCCTGACGACAACTGAAGAAAGAAAGATTAAGTGGTGAT 152
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Db 231 GAATCTTGAAGAGCTAAGCCTGACGACAACTGAAGAAAGAAAGATTAAGTGGTGAT 290
QY 153 TGTGAAGAGACATAGAGACACATGTAAGTGGAATTTGTAAGGCGGAAAGTAACCTT 212
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Db 291 TGTGAAGAGACATAGAGAGACATGTAAGTGGAATTTGTAAGGCGGAAAGTAACCTT 350
QY 213 ATGCATTTGTAATTT 227
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Db 351 ATCAAGAAAGAAATCT 365

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; Sequence 1, Application US/09765555
; Publication No. US20030037355A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Methods and compositions to modulate
; FILE REFERENCE: 27801-20014.40
; CURRENT APPLICATION NUMBER: US/09/765,555
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 09/620,897
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,468
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter CSVWV
US-09-765-555-1

Query Match 26.1%; Score 120.6; DB 9; Length 532;
Best Local Similarity 93.3%; Pred. No. 1.8e-26;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGAGCTAAGCCTGACGACAACTGAAGAAAGAAAGATTAAGTGGTGAT 152
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Db 231 GAATCTTGAAGAGCTAAGCCTGACGACAACTGAAGAAAGAAAGATTAAGTGGTGAT 290
QY 153 TGTGAAGAGACATAGAGACACATGTAAGTGGAATTTGTAAGGCGGAAAGTAACCTT 212
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Db 291 TGTGAAGAGACATAGAGAGACATGTAAGTGGAATTTGTAAGGCGGAAAGTAACCTT 350
QY 213 ATGCATTTGTAATTT 227
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Db 351 ATCAAGAAAGAAATCT 365

RESULT 15
US-09-847-057-4/c
; Sequence 4, Application US/09847057
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GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:13:29 ; Search time 1863.88 Seconds

(Without alignments)
6232.082 Million cell updates/sec

Title: US-09-963-803-20

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 43582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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3	354.2	76.7	541	36	US-09-963-803-24
4	314	68.0	341	36	US-09-963-803-19
5	262	56.7	604	36	US-09-963-803-23
6	240.2	52.0	392	36	US-09-963-803-21
7	212.4	46.0	317	36	US-09-963-803-3
8	212.4	46.0	472	36	US-09-963-803-25
9	200.4	43.4	348	36	US-09-963-803-4
10	152.8	33.1	371	36	US-09-963-803-5
11	140.8	30.5	301	36	US-09-963-803-7
12	140.8	30.5	398	36	US-09-963-803-6
13	120.6	26.1	392	1	PCT-US97-10376-1
14	120.6	26.1	392	1	PCT-US97-10376-1
15	120.6	26.1	392	16	US-09-202-838-1
16	120.6	26.1	392	16	US-09-202-838-1
17	120.6	26.1	411	1	PCT-US97-10376-4
18	120.6	26.1	411	1	PCT-US97-10376-4
19	120.6	26.1	411	16	US-09-202-838-4
20	120.6	26.1	411	16	US-09-202-838-4
21	120.6	26.1	515	25	US-09-641-466-1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22 120.6 26.1 515 36 US-09-963-803-2 Sequence 2, Appl1
23 120.6 26.1 524 1 PCT-US97-10376-2 Sequence 2, Appl1
24 120.6 26.1 524 1 PCT-US97-10376A-2 Sequence 2, Appl1
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26 120.6 26.1 524 16 US-09-202-838-3 Sequence 3, Appl1
27 120.6 26.1 524 16 US-09-202-838A-2 Sequence 2, Appl1
28 120.6 26.1 524 16 US-09-202-838A-3 Sequence 3, Appl1
29 120.6 26.1 526 1 PCT-US97-10376-3 Sequence 3, Appl1
30 120.6 26.1 526 1 PCT-US97-10376A-3 Sequence 1, Appl1
31 120.6 26.1 532 30 US-09-675-555-1 Sequence 19, Appl1
32 120.6 26.1 838 26 US-09-673-274A-19 Sequence 2, Appl1
33 120.6 26.1 853 25 US-09-641-466-2 Sequence 20, Appl1
34 120.6 26.1 1036 26 US-09-673-274A-20 Sequence 4, Appl1
35 120.6 26.1 8340 32 US-09-847-057-4 Sequence 4, Appl1
36 120.6 26.1 8340 33 US-09-847-926-4 Sequence 5, Appl1
37 120.6 26.1 12241 35 US-09-948-138-4 Sequence 5, Appl1
38 120.6 26.1 12241 38 US-10-033-190-5 Sequence 5, Appl1
39 120.6 26.1 12241 38 US-10-033-190-5 Sequence 5, Appl1
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41 117.4 25.4 305 1 PCT-US97-10376A-5 Sequence 5, Appl1
42 117.4 25.4 305 16 US-09-202-838-5 Sequence 5, Appl1
43 117.4 25.4 305 16 US-09-202-838A-5 Sequence 5, Appl1
44 117.4 25.4 420 1 PCT-US97-10376-9 Sequence 9, Appl1
45 117.4 25.4 420 1 PCT-US97-10376A-9 Sequence 9, Appl1
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ALIGNMENTS

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RESULT 1
US-09-963-803-20
Sequence 20, Application US/09963803
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 462
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter Mpr1163
NAME/KEY: promoter
LOCATION: (1)..(462)
OTHER INFORMATION:
US-09-963-803-20
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Query Match 100.0%; Score 462; DB 36; Length 462;
Best Local Similarity 100.0%; Pred. No. 4.4e-123;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 AACCTTGCATGCTGCAGCAGCTAGTATCCGCCGTCAATGACATCAGTACTGA 60
QY 61 GGAGATGAATAGCTAGCAGCAGCTGNGGAATATTGAAGACCTAAGCAGTACGAC 120
DB 61 GGAGATGAATAGCTAGCAGCAGCTGNGGAATATTGAAGACCTAAGCAGTACGAC 120
QY 121 AACCAATGAAGAAGAGAATAGGTGCTGATTTGTAAGAGAGACATAGAGACATGTA 180
DB 121 AACCAATGAAGAAGAGAATAGGTGCTGATTTGTAAGAGAGACATAGAGACATGTA 180
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QY 181 AGGTGGAATAATGTAAGCGCGGAAGTAACCTTATGCAATTTGGTTAGCAGTACT 240
DB 181 AGGTGGAATAATGTAAGCGCGGAAGTAACCTTATGCAATTTGGTTAGCAGTACT 240
QY 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTACGTAAGGATGACGATGCC 300
DB 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTACGTAAGGATGACGATGCC 300
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QY 361 ACAGATGCAAGCTTACCGCGTATCCGGTCCCAACCTTATTTCTTAATTAAGCATT 420
DB 361 ACAGATGCAAGCTTACCGCGTATCCGGTCCCAACCTTATTTCTTAATTAAGCATT 420
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DB 421 GTGTAGTACCTTGAAGAACCAACCAACCAACCAACCTTAAGGATCC 462
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RESULT 2
US-09-963-803-22
Sequence 22, Application US/09963803
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 600
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter Mpr1165
NAME/KEY: promoter
LOCATION: (1)..(600)
OTHER INFORMATION:
US-09-963-803-22
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Query Match 80.9%; Score 373.6; DB 36; Length 600;
Best Local Similarity 95.3%; Pred. No. 2.1e-97;
Matches 385; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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QY 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTACGTAAGGATGACGATGCC 300
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RESULT 3

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US-09-963-803-24
; Sequence 24, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow n
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1168
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(541)
; OTHER INFORMATION:
; US-09-963-803-24

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Query Match	76.78;	Score 354.2;	DB 36;	Length 541;
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QY	198	GCGGAAAGTAACTTATGCAATTTGTAATTTGGTTACGACTAGTAGATTGATGTATCAA	257
Db	279	GCGGAAAGTAACTTATGCAATTTGTAATTTGGTTACGACTAGTAGATTGATGTATCAA	338
QY	258	GATTGATGTGATATCTCCACGAGCGTAAAGGATAGACCATGACACACTGTGATATGATG	317
Db	339	GATTGATGTGATATCTCCACGAGCGTAAAGGATAGACCATGACACACTGTGATATGATG	398
QY	318	TGATATCAAGATTGATGTGATATCTCCACGAGCGTAAAGGATAGACCATGACCGATTAC	377
Db	399	TGATATCAAGATTGATGTGATATCTCCACGAGCGTAAAGGATAGACCATGACCGATTAC	458
QY	378	CGGTATCCCGGTTCCCAAGCTTATATTTCCTTAATTTAAGCACTGTGTAGTAGCTTAGAAA	437
Db	459	CGGTATCCCGGTTCCCAAGCTTATATTTCCTTAATTTA - ACTGTGTAGTAGCTTAGAAA	516
QY	438	ACCAACACAAACACTAGAGATTC	462
Db	517	ACCAACACAAACACTAGAGATTC	541

NOTES

RESOLUT 4
US-09-963-803-19
; Sequence 19, Application US/09963803

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: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yell
: TITLE OF INVENTION: virus and cassava vein mosaic virus
: FILE REFERENCE: 184332042
: CURRENT APPLICATION NUMBER: US/09/963,803
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: FR 99/03925
: PRIOR FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: PCT IB00/00370
: PRIOR FILING DATE: 2000-10-05
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 19
: LENGTH: 393
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: promoter MPr1162
: FEATURE:
: NAME/KEY: promoter
: LOCATION: (1) ..(393)
: OTHER INFORMATION:
: US-09-963-803-19

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Query Match	68.08;	Score 314;	DB 36;	Length 393;
Best Local Similarity	85.18;	Pred. No. 3.5e-80;		
Matches 393;	Conservative 0;	Mismatches 0;	Indels 69;	Gaps 11

QY	1	AAGCTGCATCCCTGCAGCAGCATTAATATCCCGCGTCATCAATGACATCATCAAGTACTGA	60
Db	1	AAGCTGCATCCCTGCAGCAGCATTAATATCCCGCGTCATCAATGACATCATCAAGTACTGA	60
QY	61	GGAGATGAATAGTACGACCATGACACTCTGTGCGAATATGAAAGCGTAAGCACTGACGAC	120
Db	61	GGAGATGAATAGTACGACCATGACACTCTGTGCGAATATGAAAGCGTAAGCACTGACGAC	120
QY	121	AACATGAAAGAAGAAAGATTAAGTCCGTGATTTGAAAGAGCATGAGAGACACATGTA	180
Db	121	AACATGAAAGAAGAAAGATTAAGTCCGTGATTTGAAAGAGCATGAGAGACACATGTA	180
QY	181	AGGTGGAAAATGTAAAGGGCGGAAAGTAACCTTATGCATTTGTGTAATTTGGTTAGCACTAGT	240
Db	181	AGGTGGAAAATGTAAAGGGCGGAAAGTAACCTTATGCATTTGTGTAATTTGGTT	231
QY	241	GATTGATGTGATATTCAGATTGATGTGATATCTCCACTGACGTAAAGGATAGCAGCATGCC	300
Db	232	----- 231	
QY	301	ACGACTAGTAGTATGATGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG	360
Db	232	ACGACTAGTAGTATGATGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG	291
QY	361	ACGATGCCACGTTACCCCGATGCGCGGTTCCCAAGCTTATATTCCTTATTTAAGCACTT	420
Db	292	ACGATGCCACGTTACCCCGATGCGCGGTTCCCAAGCTTATATTCCTTATTTAAGCACTT	351
QY	421	GTGTAGTAGCTTAGAAAAACCAACCAACCAACCACTGAGAGATCC	462
Db	352	GTGTAGTAGCTTAGAAAAACCAACCAACCAACCACTGAGAGATCC	393

RESULT 5

```

US-09-963-803-23
/ Sequence 23, Application US/09963803
/
/ GENERAL INFORMATION:
/ APPLICANT: Meristem Therapeutics
/ TITLE OF INVENTION: Chimeric expression promoters originating from commelina yell
/ TITLE OF INVENTION: virus and cassava vein mosaic virus
/ FILE REFERENCE: 184332042
/ CURRENT APPLICATION NUMBER: US/09/963,803
/ CURRENT FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: FR 99/03925
/

```

```

; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter Mp1167
; NAME/KEY: promoter
; LOCATION: (1)..(604)
; OTHER INFORMATION:
US-09-963-803-23
```

```

Query Match          56.7%  Score 262;  DB 36;  Length 604;
Best Local Similarity 83.3%  Pred. No. 4,9e-65;
Matches 375;  Conservative 0;  Mismatches 5;  Indels 70;  Gaps 4;
```

```

QY  78 CATGACACTCTGCGAATATTGAGACGTAAGCACTGACGACACAAATGAAAGAA 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  160 CATGCCACTCTGCGCAATATTGAAAGCACTGACGACACAAATGAAAGAA 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  138 GATAGCTCGGTGATTTGTAAGAGACATAGAGACATGTAAGGTGAAAAATGTAAG 197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  220 GATTAAGCTGCGTGTATGTG-AAAGACATAGAGACACATGTAAGGTGAAAAATGTAAG 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  198 GCGGAAGTAACCTTGTGATTTGTAATTTGTTAGACATAGATTTGATTTCAA 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  279 GCGGAAGTAACCTTGTGATTTGTAATTTGTTAGACATAGATTTGATTTCAA 336
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  258 GATTGATGATATCTCCACTGACGTAGAGGATGACGATGCCA----- 301
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  337 GATTGATGATATCTCCACTGACGTAGAGGATGACGATGCCA----- 396
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  302 -----CGACTAGTAT 312
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  397 AATCAAGATTGATGATATCTCCACTGACGTAGAGGATGACGATGCCA----- 456
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  313 TGATGATATCAAGATTGATGATATCTCCACTGACGTAGAGGATGACGATGCCA 372
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  457 TGATGATATCAAGATTGATGATATCTCCACTGACGTAGAGGATGACGATGCCA 516
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  373 TTACCCGATATGCGGTTCCCAAGCTTTATTTCTTATTTAACACTTGTAGTACT 432
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  517 TTACCCGATATGCTGTTCCCAAGCTTTATTTCTTATTTA--ACTTGTAGTACT 574
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  433 AGAAAACAAACACACACACCTAGAGATCC 462
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  575 AGAAAACAAACACACACACCTAGAGATCC 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

RESULT 6
US-09-963-803-21
; Sequence 21, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 392
; TYPE: DNA
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter Mp1164
; NAME/KEY: promoter
; LOCATION: (1)..(392)
; OTHER INFORMATION:
US-09-963-803-21
```

```

Query Match          52.0%  Score 240.2;  DB 36;  Length 392;
Best Local Similarity 77.4%  Pred. No. 8,9e-59;
Matches 349;  Conservative 0;  Mismatches 33;  Indels 69;  Gaps 2;
```

```

QY  1 AAGCTTGATGCGCTGCGACACTAGTATCCCGCTCATCATGACATCATCAGACTGA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  1 AAGCTTGATGCGCTGCGACACTAGTATCCCGCTCATCATGACATCATCAGACTGA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  61 GAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGAGCTAAGCACTGAC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  61 GAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGAGCTAAGCACTGAC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  121 AACAAATGAAGAGAAAGTAAGTGGTGGTATTTGAAAGAGACATAGAGACATGTA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  121 AACAAATGAAGAGAAAGTAAGTGGTGGTATTTGAAAGAGACATAGAGACATGTA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  181 AGGTGAAATGTAAGGGGCGAAAGTAACTTATGCAATTTGTAATTTGGTACGACTAG 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  181 AGGTGAAATGTAAGGGGCGAAAGTAACTTATGCAATTTGTAATTTGGTACGACTAG 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  241 GATTGATGATATCAAGATTGATGATATCTCCACTGACGTAGAGGATGACGATGCC 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  235 -----TGGCATGCGTATGCC 250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  301 AGCACTAGTATGATGATATCAAGATTGATGATATCTCCACTGACGTAGAGGATG 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  251 TTACGTCAGTGGAGATATCAATCATCTTGTATTCACATC----- 291
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  361 AGCATGCCACGTTACCGCGTATGCCGTTCCCAAGCTTTATTTCTTATTTAAGCACT 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  292 AATCACTAGTGGTATCCCGTATGCCGTTCCCAAGCTTTATTTCTTATTTAAGCACT 351
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  421 GTGTACTAGCTTAAGAAACCAACACACAAAC 451
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  352 GTGTACTAGCTTAAGAAACCAACACACAAAC 382
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

RESULT 7
US-09-963-803-3
; Sequence 3, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 317
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter Mp1116
; NAME/KEY: Promoter
; LOCATION: (1)..(317)
; OTHER INFORMATION:
US-09-963-803-3
```



```

RESULT 13
PCT-US97-10376-1
Sequence 1, Application PC/TUS9710376
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CASSAVA VEIN MOSAIC VIRUS PROMOTERS AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 36
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/10376
FILING DATE: 20-JUN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,129
FILING DATE: 20-JUN-1996
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US97-10376-1

Query Match          26.18; Score 120.6; DB 1; Length 392
Best Local Similarity 93.3%; Pctd. No. 4,4e-24;

```

0y 93 GAAATTTGAAGACCTAGACACTGACGCACCAATGAAAGAAAGAAAGTAAGTCGTGAT 152
143 GAACTTTGAAGACCTAAGCACACTGACGCACCAATGAAAGAAAGAAAGTAAGTCGTGAT 202
0y 153 TGTGAAAGACACATAGAGGACACATGTAAAGTGGAAAATGTAAAGCGCGGAAAGTAACCTT 212

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:19:51 ; Search time 365.79 Seconds

(without alignments)
5404.014 Million cell updates/sec

Title: US-09-963-803-20

Perfect score: 462

Sequence: 1 aagcttgatgcgcgcagca.....cacacaacctagagatcc 462

Scoring table: IDENTITY_NUC

Searched: 5824060 seqs, 2139321184 residues

Total number of hits satisfying chosen parameters: 11648120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Pending_Patents_NA_New: *
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2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq: *
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq: *
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq: *
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11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120.6	26.1	532	US-09-765-555A-1	Sequence 1, Appl
2	120.6	26.1	838	US-09-673-274B-19	Sequence 19, Appl
3	120.6	26.1	1036	US-09-673-274B-20	Sequence 20, Appl
4	40.4	8.7	309	US-10-380-935-30	Sequence 30, Appl
5	40.4	8.7	522	US-10-380-935-37	Sequence 37, Appl
6	40.4	8.7	835	US-10-391-414-10	Sequence 10, Appl
7	40.4	8.7	1683	US-60-434-166-147	Sequence 147, App
8	40.4	8.7	2361	US-10-302-267-1	Sequence 1, Appl
9	40.4	8.7	3212	US-10-130-150-13	Sequence 13, Appl
10	40.4	8.7	3288	US-10-130-150-18	Sequence 18, Appl
11	40.4	8.7	3329	US-10-130-150-15	Sequence 15, Appl
12	40.4	8.7	5247	US-10-160-764-40	Sequence 40, Appl
13	40.4	8.7	5250	US-10-160-764-4	Sequence 4, Appl
14	40.4	8.7	5511	US-10-160-764-48	Sequence 48, Appl
15	40.4	8.7	5715	US-10-160-764-52	Sequence 52, Appl
16	40.4	8.7	5796	US-10-378-810-2	Sequence 2, Appl
17	40.4	8.7	6285	US-10-160-764-42	Sequence 42, Appl
18	40.4	8.7	6299	US-10-160-764-50	Sequence 50, Appl
19	40.4	8.7	8349	US-10-198-478-16	Sequence 16, Appl
20	40.4	8.7	10249	US-10-198-478-14	Sequence 14, Appl
21	40.4	8.7	10312	US-10-198-478-15	Sequence 15, Appl
22	40.4	8.7	10339	US-10-198-478-13	Sequence 13, Appl

c	23	40.4	8.7	13737	6	US-09-538-414-10	Sequence 10, Appl
	24	39.8	8.6	250715	7	US-09-949-016-13294	Sequence 13294, A
	25	38.8	8.4	206	7	US-10-204-889-9	Sequence 9, Appl
	26	38.8	8.4	382	1	PCT-US02-17853-22	Sequence 22, Appl
	27	38.8	8.4	842	1	US-10-321-434-6	Sequence 6, Appl
	28	38.8	8.4	2267	1	PCT-US02-17853-11	Sequence 11, Appl
	29	38.8	8.4	2873	1	PCT-US03-03435-55	Sequence 55, Appl
	30	38.8	8.4	2873	9	US-10-353-454-38	Sequence 38, Appl
	31	38.8	8.4	2873	9	US-10-356-088-55	Sequence 55, Appl
	32	38.8	8.4	3002	9	US-10-353-454-57	Sequence 57, Appl
	33	38.8	8.4	3034	1	PCT-US03-03435-48	Sequence 48, Appl
	34	38.8	8.4	3034	9	US-10-353-454-31	Sequence 31, Appl
	35	38.8	8.4	3034	9	US-10-356-088-48	Sequence 48, Appl
	36	38.8	8.4	4182	5	US-09-921-922A-7	Sequence 7, Appl
	37	38.8	8.4	5449	1	PCT-US03-03435-57	Sequence 57, Appl
	38	38.8	8.4	5449	9	US-10-353-454-40	Sequence 40, Appl
	39	38.8	8.4	5449	9	US-10-356-088-57	Sequence 57, Appl
	40	38.8	8.4	6975	6	US-09-464-528C-17	Sequence 17, Appl
	41	38.8	8.4	9555	5	US-09-921-922A-6	Sequence 6, Appl
	42	38.8	8.4	13199	9	US-10-137-325A-2	Sequence 2, Appl
c	43	38.8	8.4	17476	8	US-10-385-546-7	Sequence 7, Appl
	44	37	8.0	5195	9	US-10-311-455-893	Sequence 893, App
	45	37	8.0	6944	9	US-10-311-506-113	Sequence 113, App

ALIGNMENTS

RESULT 1
US-09-765-555A-1
; Sequence 1, Application US/09765555A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Barbas, Carlos
; APPLICANT: Stege, Justin
; APPLICANT: Guan, Xueni
; APPLICANT: Dalmia, Bipin
; TITLE OF INVENTION: Methods and compositions to modulate
; FILE REFERENCE: expression in plants
; CURRENT APPLICATION NUMBER: US/09/765,555A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 09/620,897
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/177,468
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter Csywv
US-09-765-555A-1

Query Match 26.1%; Score 120.6; DB 6; Length 532;
Best local similarity 93.3%; Pred. 1.4e-25;
Matches 126; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY	93	GAATATTGAGACGTAAAGCCTGACGACACATGAAAAAGAAAGATAGTCGCGAT	132
DB	231	GAATCTTGAAGACGTAAAGCCTGACGACACATGAAAAAGAAAGATAGTCGCGAT	290
QY	153	TGTGAAAGACATAGACACATGTAAGTGAATATTAAGCGCGAAATTAACCTT	212
DB	291	TGTGAAAGACATAGACACATGTAAGTGAATATTAAGCGCGCGAAATTAACCTT	350
QY	213	ATGCATTGTAATTT	227
DB	351	ATGCATTGTAATTT	365

```

: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic oligonucleotide
: FEATURE:
: NAME/KEY: promoter
: LOCATION: (7)...(532)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (539)...(736)
: FEATURE:
: NAME/KEY: terminator
: LOCATION: (767)...(1030)
US-09-673-274B-20

Query Match          26.1%; Score 120.6; DB 6; Length 1036;
Best Local Similarity 93.38; Pred. No. 1.7e-25;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY      93 GAATATTGAACAGCTAAGCACTGACGACACAAATGAAAAGAAGAAATAGGTGGTGAT 152
         ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      222 GAATCTTGAAGACGTAAACACTGACGACACAAATGAAAAGAAGAAATAGGTGGTGAT 281

OY      153 TGTGAAGAAGCATTAAGAGCACATGTAAAGTCGAAAAATGTAAGGCCGCGAAAGTAACCTT 212
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      282 TGTGAAAAGACATTAAGAGCACATGTAAAGTTGAAAATGTAAGGCCGCGAAAGTAACCTT 341

OY      213 ATGCATTTGTATT 227
         || | || | |
DB      342 ATCACAAGAAGATCT 356

RESULT 4
US-10-380-935-30
: Sequence 30, Application US/10380935
: GENERAL INFORMATION:
: APPLICANT: WARNER, Simon, Anthony, James
: APPLICANT: HAWKES, Timothy, Robert
: APPLICANT: ANDREWS, Christopher, John
: TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
: FILE REFERENCE: PPD50594/MO
: CURRENT APPLICATION NUMBER: US/10/380.935
: CURRENT FILING DATE: 2003-03-19
: PRIOR APPLICATION NUMBER: GB002911.1
: PRIOR FILING DATE: 2000-09-29
: PRIOR APPLICATION NUMBER: GB0027693.1
: PRIOR FILING DATE: 2000-11-13
: PRIOR APPLICATION NUMBER: GB002910.3
: PRIOR FILING DATE: 2000-09-29
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
: LENGTH: 309
: TYPE: DNA
: ORGANISM: Cauliflower Mosaic Virus
: FEATURE:
: OTHER INFORMATION: Enhancer
US-10-380-935-30

Query Match          8.7%; Score 40.4; DB 8; Length 309;
Best Local Similarity 88.0%; Pred. No. 0.071;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY      258 GATGATATGATATCTCCACTGACGTAGGATGACGCATGCCACGACTA 307
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      242 GATGATATGATATCTCCACTGACGTAGGATGACGCATGCCACGACTA 291

RESULT 5
US-10-380-935-37
: Sequence 37, Application US/10380935
: GENERAL INFORMATION:
: APPLICANT: WARNER, Simon, Anthony, James
: APPLICANT: HAWKES, Timothy, Robert

```



```

; APPLICANT: ANDREWS, Christopher, John
; TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: PPD050594/NO
; CURRENT APPLICATION NUMBER: US/10/380,935
; CURRENT FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: GB0023911.1
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: GB0027693.1
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: GB0023910.3
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Figwort Mosaic Virus
; FEATURE:
; OTHER INFORMATION: Enhancer
US-10-380-935-37
```

```

Query Match          8.7%; Score 40.4; DB 8; Length 522;
Best Local Similarity 88.0%; Pred. No. 0.083;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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```
OY 258 GATTGATGATATCTCCACTGACGTAAGGATGAGCATGCCACGACTA 307
DB 459 GATTGATGATATCTCCACTGACGTAAGGATGAGCATGCCACGACTA 508
```

```

RESULT 6
US-10-391-414-10
; Sequence 10, Application US/10391414
; GENERAL INFORMATION:
; APPLICANT: SHINOZAKI, Kazuko
; APPLICANT: KATSURA, Koji
; APPLICANT: ITO, Yusuke
; TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
; FILE REFERENCE: 382.1041
; CURRENT APPLICATION NUMBER: US/10/391,414
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: JP 2002-377316
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 835
; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-10-391-414-10
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Query Match          8.7%; Score 40.4; DB 8; Length 835;
Best Local Similarity 88.0%; Pred. No. 0.096;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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OY 258 GATTGATGATATCTCCACTGACGTAAGGATGAGCATGCCACGACTA 307
DB 729 GATTGATGATATCTCCACTGACGTAAGGATGAGCATGCCACGACTA 778
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```

RESULT 7
US-60-434-166-147
; Sequence 147, Application US/60434166
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology
; APPLICANT: Creelman, Robert A.
; APPLICANT: Haake, Volker
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Adam, Luc J.
; APPLICANT: Jlang, Cal-Zhong
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Riechmann, Jose Luis
```

```

; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0051 P
; CURRENT APPLICATION NUMBER: US/60/434,166
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 559
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G2227
US-60-434-166-147
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Query Match          8.7%; Score 40.4; DB 11; Length 1683;
Best Local Similarity 88.0%; Pred. No. 0.12;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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OY 258 GATTGATGATATCTCCACTGACGTAAGGATGAGCATGCCACGACTA 307
DB 9 GATTGATGATATCTCCACTGACGTAAGGATGAGCATGCCACGACTA 58
```

```

RESULT 8
US-10-302-267-1
; Sequence 1, Application US/10302267
; GENERAL INFORMATION:
; APPLICANT: Keddie, James
; APPLICANT: Fromm, Michael
; APPLICANT: Heard, Jacqueline
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc
; APPLICANT: Broun, Pierre
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, Lynne
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jlang, Cal-Zhong
; APPLICANT: Samaha, Raymond
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Creelman, Robert
; TITLE OF INVENTION: PLANT GENE SEQUENCES II
; FILE REFERENCE: MBI-0007
; CURRENT APPLICATION NUMBER: US/10/302,267
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US/09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/120,880
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/121,037
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 60/124,278
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: 60/129,450
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/135,134
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/144,153
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/161,143
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/162,656
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2361
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: CDS
; LOCATION: (144)..(2024)
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; OTHER INFORMATION: G274
US-10-302-267-1
Query Match      8.7%; Score 40.4; DB 9; Length 2361;
Best Local Similarity 88.0%; Pred. No. 0.13;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGATGAGCATGCCAGCACTA 307
      |||||||
Db 113 GATTGATGTGATATCTCCAGCTAGAGGATGATGAGCATGCCAGCACTA 162

RESULT 9
US-10-130-150-13
; Sequence 13, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein
US-10-130-150-13

Query Match      8.7%; Score 40.4; DB 9; Length 3212;
Best Local Similarity 88.0%; Pred. No. 0.14;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGATGAGCATGCCAGCACTA 307
      |||||||
Db 197 GATTGATGTGATATCTCCAGCTAGAGGATGATGAGCATGCCAGCACTA 246

RESULT 10
US-10-130-150-18
; Sequence 18, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein fused t
; OTHER INFORMATION: and ER retaining signal peptides
US-10-130-150-18

Query Match      8.7%; Score 40.4; DB 9; Length 3288;
Best Local Similarity 88.0%; Pred. No. 0.14;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGATGAGCATGCCAGCACTA 307
      |||||||
Db 197 GATTGATGTGATATCTCCAGCTAGAGGATGATGAGCATGCCAGCACTA 246

RESULT 11
US-10-130-150-15
; Sequence 15, Application US/10130150
; GENERAL INFORMATION:
```

```
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THER
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 3329
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein fuse
; OTHER INFORMATION: signal peptide
US-10-130-150-15

Query Match      8.7%; Score 40.4; DB 9; Length 3329;
Best Local Similarity 88.0%; Pred. No. 0.14;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGATGAGCATGCCAGCACTA 307
      |||||||
Db 197 GATTGATGTGATATCTCCAGCTAGAGGATGATGAGCATGCCAGCACTA 246

RESULT 12
US-10-160-764-40
; Sequence 40, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailifoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 40
; LENGTH: 5247
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; OTHER INFORMATION: pBI121-35S-AtFPA
US-10-160-764-40

Query Match      8.7%; Score 40.4; DB 9; Length 5247;
Best Local Similarity 88.0%; Pred. No. 0.16;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGATGAGCATGCCAGCACTA 307
      |||||||
Db 3209 GATTGATGTGATATCTCCAGCTAGAGGATGATGAGCATGCCAGCACTA 3258

RESULT 13
US-10-160-764-4
; Sequence 4, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailifoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
```

```
; TITLE OF INVENTION: In Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5250
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-4

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 9; Length 5250;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCCACGACTA 307
Db 3209 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCACAAATCCACTA 3258

RESULT 14
US-10-160-764-48
; Sequence 48, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailfoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: In Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 5511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-48

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 9; Length 5511;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCCACGACTA 307
Db 3209 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCACAAATCCACTA 3258

RESULT 15
US-10-160-764-52
; Sequence 52, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailfoux, Maryse
; APPLICANT: Wang, Yang
```

```
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: In Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 5715
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-52

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 9; Length 5715;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCCACGACTA 307
Db 3209 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCACAAATCCACTA 3258
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Job time : 377.79 secs

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 06:53:52 ; Search time 1073.87 Seconds
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Title: US-09-963-803-20

Perfect score: 462
Sequence: 1 aagcttgctgcgcgcagca.....cacacaacctagagatcc 462

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_estl3:*
13: gb_estl4:*
14: gb_estl5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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21: em_gss_vrt:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43.8	9.5	224	17	BH746858
2	42.4	9.2	561	13	BM162517
3	41.8	9.0	964	9	AL529655
4	41.8	9.0	1101	17	CN60039G
5	41	8.9	222	13	BM161725
6	40.4	8.7	112	17	BH751161

7	40.4	8.7	142	17	BH749349
8	40.4	8.7	153	17	BH619283
9	40.4	8.7	153	17	BH747013
10	40.4	8.7	158	17	BH748291
11	40.4	8.7	165	17	BH747357
12	40.4	8.7	175	17	BH746616
13	40.4	8.7	177	17	BH802465
14	40.4	8.7	190	17	BH752801
15	40.4	8.7	193	17	BH748289
16	40.4	8.7	214	17	BH747829
17	40.4	8.7	215	17	BH753813
18	40.4	8.7	219	17	BH747744
19	40.4	8.7	220	17	BH747438
20	40.4	8.7	221	17	BH802415
21	40.4	8.7	230	17	BH746474
22	40.4	8.7	230	17	BH799173
23	40.4	8.7	237	17	BH802463
24	40.4	8.7	244	17	BH746375
25	40.4	8.7	248	17	BH754798
26	40.4	8.7	251	17	BH750171
27	40.4	8.7	254	17	BH748500
28	40.4	8.7	256	17	BH748499
29	40.4	8.7	258	17	BH802470
30	40.4	8.7	261	17	BH802493
31	40.4	8.7	268	17	BH611919
32	40.4	8.7	269	17	BH211646
33	40.4	8.7	269	17	BH802489
34	40.4	8.7	271	17	BH799178
35	40.4	8.7	272	17	BH802428
36	40.4	8.7	274	17	BH802495
37	40.4	8.7	279	17	BH748475
38	40.4	8.7	281	17	BH750170
39	40.4	8.7	281	17	BH802443
40	40.4	8.7	284	17	BH213307
41	40.4	8.7	284	17	BH746665
42	40.4	8.7	286	17	BH747007
43	40.4	8.7	293	17	BH610310
44	40.4	8.7	296	17	BH213532
45	40.4	8.7	335	17	BH213230

ALIGNMENTS

RESULT 1
LOCUS BH746858
DEFINITION SALK_003694.51.40.x Arabidopsis thaliana TDMN insertion lines
Arabisopsis thaliana genomic clone SALK_003694.51.40.x. DNA
sequence.
Accession BH746858
Version BH746858.1 GI:18959973
Keywords GSS.
Source thale cress.
Organism Arabidopsis thaliana

REFERENCE
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadlinb
C., Jeske,A., Kanes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J., and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker

TITLE
JOURNAL COMMENT
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckere@salk.edu

This is single pass sequence recovered from the left border of

OY	118	GACAAATGAAAAGACAAGATAAGCTCGGTGATTGGAAAAGACACTAGACACACAT	177
Db	758	RWADDRTWDRODDDDDRDRAAGTAGRKMWRPTWKRRMRKRPJMDADADADTARDRRRRRDD	699
OY	178	GTAAGGTGGAAANAATGGAAGGGCGGAAAGCACTAACCCTATGCATTTCGTAATTTGGTTCCGACT	237
Db	698	GADCKGKKTKTGKRRRRRRRARATWDRIDAWDAAMWTDTDDTDDBDKDRRKGRARRRR	639
OY	238	AGTGAATGATGATATCAGAATGATGATATGCCACTGACGACCTAAGCATGACGCAT	297
Db	638	TTRARAAMWMTWAKMADMKMKMTKTADRWDRNAADTTWTDARKADDMKARAWRRRORA	579
OY	298	GCCACGACTAGCTGATTGATGATGATATCAAGATTGATGTGATATCT	342
Db	578	RAARADRRTTKGKTATTATTTWAARAAMAAMAWATTATWT TT	534
RESULT 5			
LOCUS	BMI61725	222 bp	mRNA linear EST 04-DEC-2001
DEFINITION	EST564248 PYBS Plasmodium yoelii yoeiii cDNA clone pYCR131 5' end,		
LOCATION	BMI61725		
ACCESSION	BMI61725.1	GI:17307406	
VERSION			
KEYWORDS	EST.		
SOURCE	Plasmodium yoelii yoeiii.		
ORGANISM	Plasmodium yoelii yoeiii		
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.		
AUTHORS	Carlton,M., Daly,T.M., Long,C.A., Bergman,L.W., Valdy,A.B., Fraser,C.M. and Carucci,D.J.		
JOURNAL	Plasmodium yoelii EST project at TIGR		
COMMENT	Unpublished (2001)		
	Contact: Jane Carlton		
	Parasite Genomics Group		
	The Institute for Genomic Research		
	9712 Medical Center Drive, Rockville, MD 20850, USA		
	Tel: 301-530-9319		
	Fax: 301-838-0208		
	Email: carlton@tigr.org		
	For clone info, please contact the Malaria Research and Reference		
	Reagent Resource Center, ATCC		
	http://www.malaria.mr4.org/mr4pages/index.html		
	Seq primer: ADF.		
FEATURES			
source	location/Qualifiers		
	1..222		
	/organism="Plasmodium yoelii yoeiii"		
	/strain="17XL"		
	/db_xref="taxon:73239"		
	/clone="PYCR131"		
	/clone_lib="pyBS"		
	/dev_stage="asexual blood stages"		
	/lab_host="E. coli XL-1 Blue"		
	/note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cBYJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HyriZap arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (PAD-GAL4) was excised from the HyriZap vector and plasmid DNA isolated."		
BASE COUNT	99 a	25 c	38 g
ORIGIN			60 t

	Query Match	Best Local Similarity	Score 41;	DB 13;	Length 222;
	Matches 86;	Conservative 0;	Mismatches 75;	Indels 0;	Gaps 0;
QY	88	TGTGCGAATATTGAAGACGTAAAGCAGCTACGCAACAATGAAAAAGAGAGTAAGTCTG	147		
	11		11	11	11
Db	10	TGTAAAAAGATAGAGTATATATATTAACAACAACAGCTCGTGTGAATAATTAACCAAAATCG	69		
QY	148	GTGATTGTGAAAGAGACATACAGACACATGTAAAGGTGGAATAATTAAGGGCGAAAGTA	207		
	11		11	11	11
Db	70	GAATTTAAGAAATGGCCCTACAGGTACATATAAATGAATAGAAATCAAAAGTCGAATGAA	129		
QY	208	ACCTTATGCATTGTAAATTTGGTTACGACTAGTGGTGTG	248		
	11		11	11	11
Db	130	GGCGAAGCANTCATATTATATTATATGCTTATTTATTTATG	170		

LOCUS	112 bp	DNA	linear	GSS	27-FEB-2002
DEFINITION	BH751161				
	SALK_049464.49.75.x	Arabidopsis thaliana	YDUA insertion	lines	
	Arabidopsis thaliana	genomic clone	SALK_049464.49.75.x,	DNA	
	sequence.				

ACCESSION	BH751161	GI:18968302
KEYWORD	BH751161.1	
WORDS	GSS.	
SOURCE	thale cress.	
ORGANISM	Arabidopsis thaliana	

REFERENCE

AUTHORS • Alonso, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L., Shinn, P.

TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL	Unpublished (2001)
COMMENT	Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel.: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

```

Class: TDNA tagged.
FEATURES
    source          1. .112
    Location/Qualifiers

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/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_049464.49.75.x"
/clone_11b="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna\_protocols.html"

```

Query Match	8.7%	Score 40.4	DB 17	Length 112
Best Local Similarity	88.0%	Pred. No. 2.8		
Matches 44	Conservative	0	Mismatches 6	Indels 0
				Gaps 0

Oy 258 GATTGATGTGATATATCTCCACCTGACCGTAAGGGATGACCCATGCCACGACTA 307
 |||||
 Db 3 GATTGATGTGATATATCTCCACCTGACCGTAAGGGATGACCCATGCCACGACTA 52

RESULT 7					
BH749349		142 bp	DNA	linear	GSS 27-FEB-2002
LOCUS					
DEFINITION	BH749349				
	SLK_047736.48.15.x Arabidopsis thaliana TDNA insertion lines				

ACCESSION	BH749349	GI:18964144
VERSION	BH749349.1	
KEYWORDS	GSS.	
SOURCE	thale cress.	
ORGANISM	Arabidopsis thaliana	

REFERENCE
AUTHORS
Alonso, J. M., Leisner, T. J., Barajas, P., Chen, H., Cheuk, R., Gadrinab

TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL	Unpublished (2001)
COMMENT	Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 550 6370

Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
T-DNA.

FEATURES	Location/Qualifiers
source	1. 142

/colonyname="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_047736.48.15.x"
 /clone.lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html

Query Match Similarity 8.7%; Score 40.4; DB 17; Length 142;
Best Local Similarity 88.0%; Pred. No. 2.9;
Matches 44; Conservative 6; Indels 0; Gaps 0;

Qy 258 GATTGATGTGATATCTCCACGACCGTAAGGGATGACGCATGCCACGACTA 3077
|||||
Db 33 GATTGATGTGATATCTCCACGACCGTAAGGGATGACGCACATCCACACTA 82
|||||

RESULT 8	BH619283/c	LOCUS	DEFINITION
BH619283	153 bp	DNA	linear
SLMK_040762	Arabidopsis thaliana	TMNA insertion lines	GSS 30-JAN-2002
thaliana genomic clone SLMK_040762,	DNA sequence.		

ACCESSION	BH619283	GI:18429799
VERSION	BH619283.1	
KEYWORDS	GSS.	
SOURCE	thale cress.	
ORGANISM	Arabidopsis thaliana	

REFERENCE
AUTHORS

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae: eustosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 153)

Alonso J.M., Leisse T.J., Barajas P., Chen H., Cheuk R., Gadri nab C., Jeske A., Karnes M., Kim C.J., Parker H., Predits L., Shinn P.

QY 258 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 307
 |||||||
 DB 110 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 61

RESULT 11
 BH747357 165 bp DNA linear GSS 27-FEB-2002
 LOCUS SALK_016522.55.50.x Arabidopsis thaliana TDNA insertion lines
 DEFINITION Arabidopsis thaliana genomic clone SALK_016522.55.50.x, DNA
 sequence.

ACCESSION BH747357
 VERSION BH747357.1 GI:18960472
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana

REFERENCE
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab,
 C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)

TITLE
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

COMMENT
 This is single pass sequence recovered from the left border of
 TDNA.

FEATURES
 Class: TDNA tagged.
 Location/Qualifiers
 1..165
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_016522.55.50.x"
 /note="lib-Arabidopsis thaliana TDNA insertion lines"
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html

BASE COUNT
 45 a 43 c 39 g 38 t

Query Match 8.7%; Score 40.4; DB 17; Length 165;
 Best Local Similarity 88.0%; Pred. No. 2.9;
 Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 307
 |||||||
 DB 34 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 83

RESULT 12
 BH746616 175 bp DNA linear GSS 27-FEB-2002
 LOCUS SALK_045268.54.50.x Arabidopsis thaliana TDNA insertion lines
 DEFINITION Arabidopsis thaliana genomic clone SALK_045268.54.50.x, DNA
 sequence.

ACCESSION BH746616
 VERSION BH746616.1 GI:18959731
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana

REFERENCE
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab,
 C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)

TITLE
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

COMMENT
 This is single pass sequence recovered from the left border of
 TDNA.

FEATURES
 Class: TDNA tagged.
 Location/Qualifiers
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 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_045268.54.50.x"
 /note="lib-Arabidopsis thaliana TDNA insertion lines"
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html

BASE COUNT
 54 a 43 c 40 g 38 t

Query Match 8.7%; Score 40.4; DB 17; Length 175;
 Best Local Similarity 88.0%; Pred. No. 3;
 Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 307
 |||||||
 DB 66 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 115

RESULT 13
 BH802465/c 177 bp DNA linear GSS 25-APR-2002
 LOCUS BH802465.10.y2 1008 - RescuedMu Grid 1 Zea mays genomic, DNA
 DEFINITION

ACCESSION BH802465
 VERSION BH802465.1 GI:20316614
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays

REFERENCE
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.

TITLE
 Walbot,V.
 Maize genomic sequences found using engineered RescuedMu transposon
 Unpublished (2001)
 CONTACT: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

COMMENT
 Very probable ligation site found so sequence was trimmed.
 Post-ligation sequence submitted separately.
 Plate: 1008026 row: 10
 Class: transposon-tagged.
 Location/Qualifiers

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 175)

REFERENCE
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab,
 C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)

TITLE
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

COMMENT
 This is single pass sequence recovered from the left border of
 TDNA.

FEATURES
 Class: TDNA tagged.
 Location/Qualifiers
 1..175
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_045268.54.50.x"
 /note="lib-Arabidopsis thaliana TDNA insertion lines"
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html

BASE COUNT
 54 a 43 c 40 g 38 t

Query Match 8.7%; Score 40.4; DB 17; Length 175;
 Best Local Similarity 88.0%; Pred. No. 3;
 Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 307
 |||||||
 DB 66 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 115

RESULT 13
 BH802465/c 177 bp DNA linear GSS 25-APR-2002
 LOCUS BH802465.10.y2 1008 - RescuedMu Grid 1 Zea mays genomic, DNA
 DEFINITION

ACCESSION BH802465
 VERSION BH802465.1 GI:20316614
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays

REFERENCE
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.

TITLE
 Walbot,V.
 Maize genomic sequences found using engineered RescuedMu transposon
 Unpublished (2001)
 CONTACT: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

COMMENT
 Very probable ligation site found so sequence was trimmed.
 Post-ligation sequence submitted separately.
 Plate: 1008026 row: 10
 Class: transposon-tagged.
 Location/Qualifiers

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source
1. .177
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1008 - RescueMu Grid I"
/cisue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pInuescript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmhd.iastate.edu and follow the links for
'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

BASE COUNT      39 a      38 c      47 g      53 t

ORIGIN
Query Match      8.7%; Score 40.4; DB 17; Length 177;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCAGCACTA 307
|||||
Db 118 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCAGCACTA 69

RESULT 14
LOCUS BH752801 190 bp DNA linear GSS 27-FEB-2002
DEFINITION Arabidopsis thaliana genomic clone SALK_019366.54.25.x. DNA
sequence.
ACCESSION BH752801
VERSION BH752801
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 190)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadri nab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. .190
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_019366.54.25.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
```

```
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna-protocols.html"

BASE COUNT      52 a      52 c      41 g      45 t

ORIGIN
Query Match      8.7%; Score 40.4; DB 17; Length 190;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCAGCACTA 307
|||||
Db 81 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCAGCACTA 130

RESULT 15
LOCUS BH748289 193 bp DNA linear GSS 27-FEB-2002
DEFINITION Arabidopsis thaliana genomic clone SALK_045097.54.25.x. DNA
sequence.
ACCESSION BH748289
VERSION BH748289.1 GI:18961643
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 193)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadri nab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. .193
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_045097.54.25.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna-protocols.html"

BASE COUNT      61 a      48 c      43 g      41 t

ORIGIN
Query Match      8.7%; Score 40.4; DB 17; Length 193;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCAGCACTA 307
|||||
Db 84 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCAGCACTA 133

Search completed: April 14, 2003, 10:25:44
Job time : 1075.87 secs
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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 04:10:42 ; Search time 1713.81 Seconds

(without alignments)
10186.783 Million cell updates/sec

Title: US-09-963-803-22

Perfect score: 600

Sequence: 1 aagcttgcatgcctgcagca.....cacacaactagatgcc 600

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_da: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_ph: *
24: em_pl: *
25: em_ro: *
26: em_sts: *
27: em_un: *
28: em_vi: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_mus: *
33: em_htg_other: *
34: em_htg_pln: *
35: em_htg_rtd: *
36: em_htg_mam: *
37: em_htg_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	600	100.0	600	6	AX036756	AX036756 Sequence
2	587	97.8	9285	6	AX093047	AX093047 Sequence
3	587	97.8	15077	6	AX093052	AX093052 Sequence
4	373.6	62.3	462	6	AX036754	AX036754 Sequence
5	312.2	52.0	604	6	AX036757	AX036757 Sequence
6	304.6	50.8	393	6	AX036753	AX036753 Sequence
7	281.4	46.9	541	6	AX036758	AX036758 Sequence
8	234.2	39.0	392	6	AX036755	AX036755 Sequence
9	212.4	35.4	317	6	AX036737	AX036737 Sequence
10	212.4	35.4	472	6	AX036738	AX036738 Sequence
11	200.4	33.4	348	6	AX036739	AX036739 Sequence
12	152.8	25.5	371	6	AX036741	AX036741 Sequence
13	140.8	23.5	301	6	AX036740	AX036740 Sequence
14	140.8	23.5	515	6	AX036736	AX036736 Sequence
15	120.6	20.1	515	6	AX088388	AX088388 Sequence
16	120.6	20.1	532	6	AX202413	AX202413 Sequence
17	120.6	20.1	838	6	AX014764	AX014764 Sequence
18	120.6	20.1	838	6	AX088389	AX088389 Sequence
19	120.6	20.1	1036	6	AX014765	AX014765 Sequence
20	120.6	20.1	1036	6	CV020341	CV020341 Sequence
21	120.6	20.1	8158	14	CV059751	CV059751 Sequence
22	120.6	20.1	8340	6	AX329231	AX329231 Sequence
23	120.6	20.1	8340	6	AX338536	AX338536 Sequence
24	120.6	20.1	12241	6	AX412168	AX412168 Sequence
25	120.6	20.1	593	6	AX088390	AX088390 Sequence
26	115.8	19.3	857	6	AX088391	AX088391 Sequence
27	115.8	19.3	931	6	AX088392	AX088392 Sequence
28	115.4	19.2	931	6	AX088393	AX088393 Sequence
29	115.4	19.2	931	6	AX088393	AX088393 Sequence
30	115.4	19.2	931	6	AX088393	AX088393 Sequence
31	81.4	13.6	7489	14	CY000000	CY000000 Sequence
32	80	13.3	243	6	AX036735	AX036735 Sequence
33	75.4	12.6	392	6	AX036755	AX036755 Sequence
34	69.6	11.6	79	6	AX036611	AX036611 Sequence
35	69.6	11.6	79	6	AX036748	AX036748 Sequence
36	69.6	11.6	296	6	AX036603	AX036603 Sequence
37	69	11.5	259	6	AX036616	AX036616 Sequence
38	62	10.3	62	6	AX036744	AX036744 Sequence
39	60	10.0	60	6	AX036743	AX036743 Sequence
40	60	10.0	63	6	AX036746	AX036746 Sequence
41	58	9.7	80	6	AX103782	AX103782 Sequence
42	58	9.7	236	6	AX103783	AX103783 Sequence
43	58	9.7	299	6	AX103784	AX103784 Sequence
44	58	9.7	332	6	AX103755	AX103755 Sequence
45	58	9.7	472	6	AX103753	AX103753 Sequence

ALIGNMENTS

RESULT 1
AX036756
LOCUS AX036756 600 bp
DEFINITION Sequence 22 from Patent WO058485.
ACCESSION AX036756
VERSION AX036756.1 GI:11226265
KEYWORDS
ORGANISM
SOURCE
synthetic construct.
artificial sequences.
1 (bases 1 to 600)
REFERENCE
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 22 OCT-2000.

JOURNAL


```
source 1. .15077
/organism="synthetic construct"
/db_xref="taxon:32630"
/misc_feature 1
/note="pMR1342 results from the replacement of the
expression cassette ep35S-gus-polyA35S from pMR1335 by
the expression cassette l5-gus-polyA35S isolated from
pMR1336"
BASE COUNT 3672 a 3892 c 4225 g 3288 t
ORIGIN
Query Match 97.8%; Score 587; DB 6; Length 15077;
Best Local Similarity 100.0%; Pred. No. 2.2e-150;
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 TGCCTGACGACCTAGTATCCGCGCTATCATGACATCATCATGAGATGAA 69
DB 6838 TGCCCTGACGACCTAGTATCCGCGCTATCATGACATCATGAGATGAA 6897
QY 70 TAGCTAGCCTAGCACCTCTGCGAATTTGAAGAGCTAGACCTGACCAACATGAA 129
DB 6898 TAGCTAGCCTAGCACCTCTGCGAATTTGAAGAGCTAGACCTGACCAACATGAA 6957
QY 130 AAGAGAGATAGAGTCTGATTTGTGAAGAGACATAGAGACACATGTAAGGTGAAA 189
DB 6958 AAGAGAGATAGAGTCTGATTTGTGAAGAGACATAGAGACACATGTAAGGTGAAA 7017
QY 190 ATGTAGAGGCGGAAAGTACCTTATGCAATTTGTATTTGTTACGACTAGTATGATGT 249
DB 7018 ATGTAGAGGCGGAAAGTACCTTATGCAATTTGTATTTGTTACGACTAGTATGATGT 7077
QY 250 GATATCAAGTTGATGATATCTCCACGTAGAGGATGAGCGGATGCGACAGCATAGT 309
DB 7078 GATATCAAGTTGATGATATCTCCACGTAGAGGATGAGCGGATGCGACAGCATAGT 7137
QY 310 GATTGATGATATCAAGATTTGATATCTCCACTGAGTAAAGGATAGCGATGCC 369
DB 7138 GATTGATGATATCAAGATTTGATATCTCCACTGAGTAAAGGATAGCGATGCC 7197
QY 370 ACGACTAGTATGATGATATCAAGATTTGATATCTCCACTGAGTAAAGGATG 429
DB 7198 ACGACTAGTATGATGATATCAAGATTTGATATCTCCACTGAGTAAAGGATG 7257
QY 430 ACGATGCCACGACTAGTATGATGATATCAAGATTTGATATCTCCACTGAG 489
DB 7258 ACGATGCCACGACTAGTATGATGATATCAAGATTTGATATCTCCACTGAG 7317
QY 490 TAAGGATGACGATGCCAGTTACCGGATGCGGTTCCCAAGCTTATTTCTTATT 549
DB 7318 TAAGGATGACGATGCCAGTTACCGGATGCGGTTCCCAAGCTTATTTCTTATT 7377
QY 550 TAAGCACTTGTAGTAGCTTAGAAAACAACACACACACCTAGAGG 596
DB 7378 TAAGCACTTGTAGTAGCTTAGAAAACAACACACACACCTAGAGG 7424
RESULT 4
AX036754 462 bp DNA linear PAT 16-NOV-2000
LOCUS AX036754
DEFINITION Sequence 20 from Patent WO0058485.
ACCESSION AX036754
VERSION AX036754.1 GI:11226263
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 462)
AUTHORS
Rance, I., Theisen, M. and Gruber, V.
TITLE
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 20 05-OCT-2000;
JOURNAL
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
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FEATURES ; GRUBER VERONIQUE (FR)
source 1. .462
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter Mpr1163"
BASE COUNT 148 a 87 c 111 g 116 t
ORIGIN
Query Match 62.3%; Score 373.6; DB 6; Length 462;
Best Local Similarity 95.3%; Pred. No. 8.9e-92;
Matches 385; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 AAGCTTCATGCTCGCAGCAGCTAGTATCCCGCTGATCATATGACATATACAGTACTGA 60
DB 1 AAGCTTCATGCTCGCAGCAGCTAGTATCCCGCTGATCATATGACATATACAGTACTGA 60
QY 61 GGAGATGAATAGCTAGCAGCAGCTGTCGCAATTTGAAGACGTAAGCAGTACGAC 120
DB 61 GGAGATGAATAGCTAGCAGCAGCTGTCGCAATTTGAAGACGTAAGCAGTACGAC 120
QY 121 AACATGAAAAAAGAAAGATAGGTCGATTTGTGAAGAGACATAGAGACATGTA 180
DB 121 AACATGAAAAAAGAAAGATAGGTCGATTTGTGAAGAGACATAGAGACATGTA 180
QY 181 AGGTGGAAAAATGTAAGGCGGAAAGTAACTTATGCAATTTGTTAGTACAGCATAGT 240
DB 181 AGGTGGAAAAATGTAAGGCGGAAAGTAACTTATGCAATTTGTTAGTACAGCATAGT 240
QY 241 GATTGATGATATCAAGATTTGATATCTCCACTGAGTAAAGGATAGCGATGCC 300
DB 241 GATTGATGATATCAAGATTTGATATCTCCACTGAGTAAAGGATAGCGATGCC 300
QY 301 ACGACTAGTATGATGATATCAAGATTTGATATCTCCACTGAGTAAAGGATG 360
DB 301 ACGACTAGTATGATGATATCAAGATTTGATATCTCCACTGAGTAAAGGATG 360
QY 361 ACGATGCCACGACTAGTATGATGATATCAAGATTTGATATCTCCACTGAGTAAAGGATG 404
DB 361 ACGATGCCACGACTAGTATGATGATATCAAGATTTGATATCTCCACTGAGTAAAGGATG 404
RESULT 5
AX036757 604 bp DNA linear PAT 16-NOV-2000
LOCUS AX036757
DEFINITION Sequence 23 from Patent WO0058485.
ACCESSION AX036757
VERSION AX036757.1 GI:11226266
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 604)
AUTHORS
Rance, I., Theisen, M. and Gruber, V.
TITLE
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 23 05-OCT-2000;
JOURNAL
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
FEATURES
source 1. .604
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter Mpr1167"
BASE COUNT 186 a 116 c 145 g 157 t
ORIGIN
Query Match 52.0%; Score 312.2; DB 6; Length 604;
Best Local Similarity 84.5%; Pred. No. 6.1e-75;
Matches 442; Conservative 0; Mismatches 3; Indels 78; Gaps 5;
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[illegible]

Db	61	GGAGTATGATACCTAGCCATGACACTCTGTGCGAATATTGGAAGACGTAAAGCATGACAGAC	120
Qy	121	AACAAATGAAAAGAAAGATAAAGTCGGTGTATTGTGAAAAGACATAGACACATGTA	180
Db	121	AACAAATGAAAAGAAAGATAAAGTCGGTGTATTGTGAAAAGACATAGACACATGTA	180
Qy	181	AGGTGAAAATGTAAAGGCGGAAAGTAACCTTATGCAATTTGTAAATTTGGTTACGACTAGT	240
Db	181	AGGTGAAAATGTAAAGGCGGAAAGTAACCTTATGCAATTTGTAAATTTGGTTACGACTAGT	240
Qy	241	GATTGATGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCC	300
Db	241	GATTGATGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCC	300
Qy	301	ACGACTAGTATGATGTGATATCAAGATTGATGT	335
Db	301	ACGTTACCCCGTATGCCGTTCCCAAGCTTTATT	335
RESULT 7			
LOCUS	AX036758	541 bp	DNA
DEFINITION	Sequence 24 from Patent WO0058485.		Linear
ACCESSION	AX036758		
VERSION	AX036758.1	GI:11226267	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
promoter			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 305: Conservative			
Qy	78	CATGACACTCTGTGCGAATATTGAAGACGTAAAGCACTGACGACAAATGAAAAGAA	137
Db	160	CATGCCACTCTGTGCGAATATTGAAGACGTAAAGCACTGACGACAAATGAAAAGAA	219
Qy	138	GATAAGTCGCGTGTGTAAGAGACATAGAGACACATGTAAAGTGGAAAATGTAAG	197
Db	220	GATAAGTCGCGTGTGTAAGAGACATAGAGACACATGTAAAGTGGAAAATGTAAG	278
Qy	198	GCGGAAAGAACCTTATGCAATTTGTAATTTGGTTACGACTGTGATGATGATATCA	257
Db	279	GCGGAAAGAACCTTATGCAATTTGTAATTTGGTTACGACTGTGATGATGATATCA	338
Qy	258	GATTGATGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCAGTATGATG	317
Db	339	GATTGATGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCAGTATGATG	398
Qy	318	TGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCAGTATG	377
Db	399	TGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCAGTATG	458
Qy	378	TGATGATGTGATATCAAGATTGATGT	404
Db	459	CGGTATGCTGTGTTCCCAAGCTTTATT	485

RESULT 8			
AX036755			
LOCUS	AX036755	392 bp	DNA
DEFINITION	Sequence 21 from Patent WO0058485.		linear
ACCESSION	AX036755		PAT 16-NOV-2000
VERSION	AX036755.1	GI:11226264	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
promoter			
BASE COUNT			
ORIGIN			

Query Match	39.0%	Score 234.2;	DB 6;	Length 392;
Best Local Similarity	96.8%;	Pred. No. 1.5e-53;		
Matches 239; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;
OY	1	AAGCTTGCAATCCCTGACACACTAGTATCGGCCGTGCATCATGATCATCAGTACTGA	60	
Db	1	AAGCTTGATCGCTGCGACACTAGTATCGGCCGTGCATCATGACATCATCACAGTACTGA	60	
OY	61	GGAGATGTAATAGCTTAGCCATGACACTCTGTGCGAATAATTGAAGACGTAAAGCACTGACGAC	120	
Db	61	GGAGATGTAATAGCTTAGCCATGACACTCTGTGCGAATAATTGAAGACGTAAAGCACTGACGAC	120	
OY	121	AACAATGAAAAGAACAATAAAGTCGGTGATTGTGAAAAGAGACATTAAGACACATATGTA	180	
Db	121	AACAATGAAAAGAACAATAAAGTCGGTGATTGTGAAAAGAGACATTAAGACACATATGTA	180	
OY	181	AGGTGGAATAATGTAAGGCGCGAAGAAGTAACTTATGCATTTGTGATTGGTTACGACCTAGT	240	
Db	181	AGGTGGAATAATGTAAGGCGCGAAGAAGTAACTTATGCATTTGTGATTGGTTACGATGCGAT	240	
OY	241	GATTGAT	247	
Db	241	GCGTCAT	247	
RESULT 9				
LOCUS	AX036737	317 bp	DNA	linear PAT 16-NOV-2000
DEFINITION	Sequence 3 from Patent WO0058485.			
ACCESSION	AX036737			
VERSION	AX036737.1	GI:11226246		
KEYWORDS	.			
SOURCE	synthetic construct.			
ORGANISM	synthetic construct			
REFERENCE	artificial sequences.			
AUTHORS	1 (bases 1 to 317)			
TITLE	Rance,I., Theisen,M. and Gruber,V.			
JOURNAL	Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus			
	Patent: WO 0058485-A 3 05-OCT-2000;			
	MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)			
	; GRUBER VERONIQUE (FR)			
FEATURES	Location/Qualifiers			
SOURCE	1..317			
	/organism="synthetic construct"			
	/db_xref="taxon:32630"			

	promoter	/note="promoter MPrill6"
BASE COUNT	107 a 61 c 74 g 75 t	
ORIGIN		
Query Match	35.4%;	Score 212.4; DB 6; Length 317;
Best Local Similarity	99.5%;	Pred. No. 1.5e-47;
Matches 213; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
Oy	20 ACTAGTATCCGCCGCTCATCATGACATCATCATCAGTACTGAGAGATGAAATGCTAGGCCA	79
Db	18 ACTAGTATCCGCCGCTCATCATGACATCATCATCAGTACTGAGAGATGAAATGCTAGGCCA	77
Oy	80 TGACACTCTGTGTCGGAATTTGGAAGCGTAAGACGTAGACAGACAAACAATGAAAGGAAGA	139
Db	78 TGACACTCTGTGTCGGAATTTGGAAGCGTAAGACGTAGACAGACAAACAATGAAAGGAAGA	137
Oy	140 TAAGTCGGGTGATTTGGAAGAGACATAGAGACACATGTAAAGTGGAAATGTAAAGGC	199
Db	138 TAAGTCGGGTGATTTGGAAGAGACATAGAGACACATGTAAAGTGGAAATGTAAAGGC	197
Oy	200 GGAAGTAACTTATGCATTTCTAATTTCTAGTAC	233
Db	198 GGAAGTAACTTATGCATTTCTAATTTCTAGTAC	231

Result	LOCUS	DEFINITION	Accession	DNA	linear	PAT
10	AX036759	Sequence 25 from Patent WO0058485.	AX036759	472 bp		16-NOV-2000
	VERSION	AX036759.1	GI:11226268			
	KEYWORDS					
	SOURCE	synthetic construct.				
	ORGANISM	artificial sequences.				
	REFERENCE	1 (bases 1 to 472)				
	AUTHORS	Rance,I., Theisen,M. and Gruber,V.				
	TITLE	Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus				
	JOURNAL	Patent: WO 0058485-A 25 05-Oct-2000;				
		MEISTERN THEAPREUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR) ; GRUBER VERONIQUE (FR)				
	FEATURES	Location/Qualifiers				
	source	1..472				
		/organism="synthetic construct"				
		/db_xref="taxon:32630"				
		/note="Promoter MPr1169"				
	Promoter	1..472				
	BASE COUNT	149 a 92 c 112 g 119 t				
	ORIGIN					
	Query Match	35.4%: Score 212.4; DB 6; Length 472;				
	Best Local Similarity	91.5%: Pred. NO. 1.5e-47;				
	Matches 236; Conservative	0; Mismatches 21; Indels 1; Gaps 1;				
QY	78	CATGACACTCTGTGCGAATATTGAAGACGTAAAGCACTGACGACCAACATGAAAAGAA	137			
Db	160	CATGCTCTCTGTCGCAATATTGAAGACGTAAAGCACTGACGACCAACATGAAAAGAA	219			
QY	138	GATAAGTCGCGGATGTGGAAGAAGACATPAGAGACACATGTAAGTGGAAATGTAAGG	197			
Db	220	GATAAGTCGCGGATGTGGAAGAAGACATPAGAGACACATGTAAGTGGAAATGTAAGG	278			
QY	198	GCGGAAGATTAACCTTATGCAATTTGTAATTTGGTTACGACTAGTGAATGATGATATCAA	257			
Db	279	GCGGAAGATTAACCTTATGCAATTTGTAATTTGGTTACGACTAGTGAATGATGATATCAA	338			
QY	258	GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCGACAGACAGATGATTAAG	317			
Db	339	GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCGACAGATGATTAAG	398			
QY	318	TGATATCAAGATTGATGT 335				

PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
PS Claim 5; Page 86-87; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 600 BP; 188 A; 111 C; 147 G; 154 T; 0 other;
XX
Query Match 100.0%; Score 600; DB 21; Length 600;
Best Local Similarity 100.0%; Pred. NO. 9.2e-174;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCTTGATGCTGCTGACAGCTAGTATCCGCGTCATCATGACATCAGTACTGA 60
DB 1 AAGCTTGATGCTGCTGACAGCTAGTATCCGCGTCATCATGACATCAGTACTGA 60
QY 61 GGAGTGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 61 GGAGTGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 121 AACATGAAAGAAAGAAATAGTATGATGATGATGATGATGATGATGATGATGAT 180
DB 121 AACATGAAAGAAAGAAATAGTATGATGATGATGATGATGATGATGATGATGAT 180
QY 181 AGGTGGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 AGGTGGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 GATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 241 GATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 ACGACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 ACGACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 ACGCTGACGACGACTAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 ACGCTGACGACGACTAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 TAAGGATGACGATGCCAGCACTAGTATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 TAAGGATGACGATGCCAGCACTAGTATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 CCACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 CCACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 TTCCCTATTATTAAGCACTTGTAGTAGTAAACCAACAACAACAACAACAACAACA 600
DB 541 TTCCCTATTATTAAGCACTTGTAGTAGTAAACCAACAACAACAACAACAACAACA 600

RESULT 2
AAA96854
ID AAA96854 standard; DNA; 462 BP.
XX
AC AAA96854;
XX
DT 19-FEB-2001 (first entry)

XX
DE Nucleotide sequence of chimeric expression promoter MP1163.
XX
XX Promoter; Intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
XX
XX 05-OCT-2000.
XX
XX 29-MAR-2000; 2000MO-IB00370.
XX
XX 29-MAR-1999; 99FR-0003925.
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI: 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
PS Claim 5; Page 86; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 462 BP; 148 A; 87 C; 111 G; 116 T; 0 other;
XX
Query Match 62.3%; Score 373.6; DB 21; Length 462;
Best Local Similarity 95.3%; Pred. NO. 2e-104;
Matches 385; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 AAGCTTGATGCTGCTGACAGCTAGTATCCGCGTCATCATGACATCAGTACTGA 60
DB 1 AAGCTTGATGCTGCTGACAGCTAGTATCCGCGTCATCATGACATCAGTACTGA 60
QY 61 GGAGTGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 61 GGAGTGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 121 AACATGAAAGAAAGAAATAGTATGATGATGATGATGATGATGATGATGATGAT 180
DB 121 AACATGAAAGAAAGAAATAGTATGATGATGATGATGATGATGATGATGATGAT 180
QY 181 AGGTGGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 AGGTGGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 GATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 241 GATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 ACGACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 ACGACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360

CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.

SO Sequence 393 BP; 128 A; 75 C; 93 G; 97 T; 0 other;

Query Match 50.8%; Score 304.6; DB 21; Length 393;
Best Local Similarity 94.3%; Pred. No. 2.6e-83;
Matches 316; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 AACCTGATGCTGCGACGCTAGTATCCCGCTCATCAATGACATATCAGACTGCA 60
DB 1 AACCTGATGCTGCGACGCTAGTATCCCGCTCATCAATGACATATCAGACTGCA 60
QY 61 GGAGATGAATAGCTAGCAGACACCTGTGCGAATTTGAAGCCGTAACACTGACGAC 120
DB 61 GGAGATGAATAGCTAGCAGACACCTGTGCGAATTTGAAGCCGTAACACTGACGAC 120
QY 121 AACATGMAAAGAAGATAGTGGTGTGTAAGAGACATAGAGACATGTA 180
DB 121 AACATGMAAAGAAGATAGTGGTGTGTAAGAGACATAGAGACATGTA 180
QY 181 AGGTGMAAATGTAAGGCGGAAAGTAACTTATGCAATTTGTAATTTGGTTACGACTAGT 240
DB 181 AGGTGMAAATGTAAGGCGGAAAGTAACTTATGCAATTTGTAATTTGGTTACGACTAGT 240
QY 241 GATTGATGATATCAAGATTGATGTATCCCACTGACGTAAGGATGACGACATGCC 300
DB 241 GATTGATGATATCAAGATTGATGTATCCCACTGACGTAAGGATGACGACATGCC 300
QY 301 ACGACTAGTATGATGTATATCAAGATTGATGT 335
DB 301 ACGTACCCGCTATGCCGCTTCCCAAGCTTATTT 335

RESULT 5
AAA96858 standard; DNA; 541 BP.

AC AAA96858;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter Mp1168.

KM Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KW plant green tissue expression promoter; Cassava vein mosaic virus;

OS Chimeric - Commelina yellow mottle virus.

OS Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

DR WPI: 2000-647238/62.

Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region, replaced
PT with sequence from promoter comprising green tissue expression region
XX

PS Claim 5; Page 87-88; 91pp; English.

XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.

SO Sequence 541 BP; 169 A; 104 C; 130 G; 138 T; 0 other;

Query Match 46.9%; Score 281.4; DB 21; Length 541;
Best Local Similarity 93.3%; Pred. No. 3.8e-76;
Matches 305; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 78 CATGACACTGTGCGAATTTGAAGACGTAACGACGACACATGMAAAGAAGAA 137
DB 160 CATGCCACTGTGCGAATTTGAAGACGTAACGACGACACATGMAAAGAAGAA 219
QY 138 GATAGGTCGCTGATTTGTGAAGAAGACATAGAGACATGTAAGGTGMAAATGTAAG 197
DB 220 GATAGGTCGCTGATTTGTG- AAGAGACATAGAGACACATGTAAGGTGMAAATGTAAG 278
QY 198 GCGGAAAGTAACTTATGCAATTTGTAATTTGGTTACGACTAGTATGATATCA 257
DB 279 GCGGAAAGTAACTTATGCAATTTGTAATTTGGTTACGACTAGTATGATATCA 338
QY 258 GATTGATGATATTCACACTGACGTAAGGATGACGATGCCACGACTAGTATGATG 317
DB 339 GATTGATGATATTCACACTGACGTAAGGATGACGATGCCACGACTAGTATGATG 398
QY 318 TGATATCAAGATTGATGTATCTCCACTGACGTAAGGATGACGATGCCACGACTAG 377
DB 399 TGATATCAAGATTGATGTATCTCCACTGACGTAAGGATGACGATGCCACGACTAG 458
QY 378 TGATGATGATATCAAGATTGATGT 404
DB 459 CGGTATGCTGCTCCCAAGCTTATTT 485

RESULT 6
AAA96855 standard; DNA; 392 BP.

AC AAA96855;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter Mp1164.

KM Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KW plant green tissue expression promoter; Cassava vein mosaic virus;

OS Chimeric - Commelina yellow mottle virus.

OS Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERI-) MERISTEM THERAPEUTICS.

XX	29-MAR-1999;	99FR-0003925.
PR	(MERI-)	MERISTEM THERAPEUTICS.
PA	Rance I,	Gruber V, Theisen M;
XX	WP1: 2000-647238/62.	
PI		
XX		
DR		
XX		
PT	Chimeric expression promoter for transgenic plant production, comprises	
PT	sequence from promoter comprising vascular expression region replaced	
PT	with sequence from promoter comprising green tissue expression region	
XX		
XX	Claim 5; page 81; 91pp; English.	
PS		
XX		
CC	The present sequence represents a chimeric promoter of the invention.	
CC	The specification describes chimeric expression promoters. These	
CC	chimeric promoters comprise a nucleic acid sequence which is derived	
CC	from a first plant promoter, in which a plant vascular expression	
CC	promoter region is replaced with a nucleic acid sequence derived from	
CC	a second plant promoter comprising a plant green tissue expression	
CC	promoter region. Preferably, the first plant promoter originates from	
CC	Commelina yellow mottle virus, and the second plant promoter originates	
CC	from the Cassava vein mosaic virus. Especially, the promoters are	
CC	derived from intergenic regions. The chimeric promoters are useful	
CC	for producing transgenic plants.	
XX		
SO	Sequence 317 BP; 107 A; 61 C; 74 G; 75 T; 0 other;	
Query Match	35.4%; Score 212.4; DB 21; Length 317;	
Best Local Similarity	99.5%; Pred. No. 4.2e-55;	
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	20 ACTAGTATCCCCCGCATCATGACATATCATCTACTGAGAGATGTAATGCTAGCCA	79
DB	18 ACTAGTATCCCCCGCATCATGACATATCATCTACTGAGAGATGTAATGCTAGCCA	77
QY	80 TGACACTCTGTGCGCAATTTTGAAGACGTAGACACTGAGACAAATGAAAAGAGA	139
DB	78 TGACACTCTGTGCGCAATTTTGAAGACGTAGACACTGAGACAAATGAAAAGAGA	137
QY	140 TAAAGTCGATGATTTGTGAAGAGACATAGAGACACATGTAGTGAAGTGAAGG	199
DB	138 TAAAGTCGATGATTTGTGAAGAGACATAGAGACACATGTAGTGAAGTGAAGG	197
QY	200 GGAAGTAACTTATGCACTTTTGTAAATTTTGCTTAC	233
DB	198 GGAAGTAACTTATGCACTTTTGTAACTTTGCTTAC	231
RESULT 8		
AAA96859	AAA96859 standard; DNA; 472 BP.	
XX	AAA96859;	
AC		
XX	19-FEB-2001 (first entry)	
DE	Nucleotide sequence of chimeric expression promoter MER1169.	
XX		
KM	Promoter: intergenic region; Commelina yellow mottle virus;	
KM	chimeric expression promoter; plant vascular expression promoter;	
KM	plant green tissue expression promoter; Cassava vein mosaic virus;	
XX	transgenic plant; chimera; ss.	
OS	Chimeric - Commelina yellow mottle virus.	
OS	Chimeric - Cassava vein mosaic virus.	
XX		
PN	WO200058485-A1.	
XX		
XX	05-OCT-2000.	


```
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
PN
XX 05-OCT-2000.
PD
XX 29-MAR-2000; 2000WO-IB00370.
PF
XX 29-MAR-1999; 99FR-0003925.
PR
XX (MERI-) MERISTEM THERAPEUTICS.
PA
XX Rance I, Gruber V, Theisen M;
PI
XX WPI; 2000-647238/62.
DR
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5; Page 81; 91pp; English.
PS
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 371 BP; 122 A; 68 C; 89 G; 92 T; 0 other;
Query Match 25.5%; Score 152.8; DB 21; Length 371;
Best Local Similarity 98.7%; Pred. No. 8.2e-37;
Matches 154; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 78 CATGACACTCTGTGCGAATATTGAAGACGTAGACGACGACAACATGAAAGAGAA 137
DB 130 CATGCACTCTGTGCGAATATTGAAGACGTAGACGACGACAACATGAAAGAGAA 189
OY 138 GATAAGTCGCGTGAATTTGGAAGACATAGAGACACATGTAAAGTGAAGTAAAG 197
DB 190 GATAAGTCGCGTGAATTTGGAAGACATAGAGACACATGTAAAGTGAAGTAAAG 249
OY 198 GCGGAAGTAACCTTATGCATTGTGTAATTGGTTAC 233
DB 250 GCGGAAGTAACCTTATGCATTGTGTAATTGGTTAC 285
RESULT 11
AAA96841
ID AAA96841 standard; DNA; 301 BP.
XX
XX AAA96841;
AC
XX 19-FEB-2001 (first entry)
DT
XX
XX Nucleotide sequence of chimeric expression promoter MPr1154.
DE
XX
XX Promoter: intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
```

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XX
XX 05-OCT-2000.
PD
XX
XX 29-MAR-2000; 2000WO-IB00370.
PF
XX 29-MAR-1999; 99FR-0003925.
PR
XX (MERI-) MERISTEM THERAPEUTICS.
PA
XX Rance I, Gruber V, Theisen M;
PI
XX WPI; 2000-647238/62.
DR
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5; Page 82; 91pp; English.
PS
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 301 BP; 98 A; 54 C; 74 G; 75 T; 0 other;
Query Match 23.5%; Score 140.8; DB 21; Length 301;
Best Local Similarity 98.1%; Pred. No. 3.6e-33;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
OY 78 CATGACACTCTGTGCGAATATTGAAGACGTAGACGACGACAACATGAAAGAGAA 137
DB 63 CATGCACTCTGTGCGAATATTGAAGACGTAGACGACGACAACATGAAAGAGAA 122
OY 138 GATAAGTCGCGTGAATTTGGAAGACATAGAGACACATGTAAAGTGAAGTAAAG 197
DB 123 GATAAGTCGCGTGAATTTG- AAGAGACATAGAGACACATGTAAAGTGAAGTAAAG 181
OY 198 GCGGAAGTAACCTTATGCATTGTGTAATTGGTTAC 233
DB 182 GCGGAAGTAACCTTATGCATTGTGTAATTGGTTAC 217
RESULT 12
AAA96840
ID AAA96840 standard; DNA; 398 BP.
XX
XX AAA96840;
AC
XX 19-FEB-2001 (first entry)
DT
XX
XX Nucleotide sequence of chimeric expression promoter MPr1147.
DE
XX
XX Promoter: intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
XX 05-OCT-2000.
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PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
PI Rance I, Gruber V, Theisen M;
XX
XX WPI; 2000-647238/52.
DR
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
PS Claim 5; Page 82; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC cornellina yellow mottle virus, and the second plant promoter originates
CC from the cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 398 BP; 128 A; 80 C; 93 G; 97 T; 0 other;

Query Match 23.5%; Score 140.8; DB 21; Length 398;
Best Local Similarity 98.1%; Pred. No. 4e-33;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 78 CATGACACTGTGCGCAATTGTAAGACGTAGCACTGACGACACATGAAAGAGAA 137
DB 160 CATGCCACTGTGCGCAATTGTAAGACGTAGCACTGACGACACATGAAAGAGAA 219
QY 138 GATAAGTCCGATGATTGTAAGACATGTAAGGTAAGGTAAGGTAAGG 197
DB 220 GATAAGTCCGATGATTGTAAGACATGTAAGGTAAGGTAAGGTAAGG 278
QY 198 GCGGAAAGTAACTTATGCAATTTGTAATTTGCTTAC 233
DB 279 GCGGAAAGTAACTTATGCAATTTGTAATTTGCTTAC 314

RESULT 13
AAV14019
ID AAV14019 standard; DNA; 392 BP.
XX
AC AAV14019;
XX
DT 18-JUN-1998 (first entry)
XX
DE CSMV promoter CVP1.
XX
KM Cassava vein mosaic virus; CSMV; promoter; cultivated crop;
KM tissue-specific expression control; transgenic plant; ss.
XX
OS Cassava vein mosaic virus.
XX
PN WO9748819-A1.
XX
PD 24-DEC-1997.
XX
PF 20-JUN-1997; 97WO-US10376.
XX
PR 20-JUN-1996; 96US-0020129.
XX
PA (SCRI) SCRIPPS RES INST.
XX

PI Beachy RN, De Kochko A, Fauquet C, Verdagner B;
XX
DR WPI; 1998-063157/06.
XX
PT Cassava vein mosaic virus promoter - used to express heterologous
PT DNA sequences for producing transgenic plants having altered
PT phenotype(s)
XX
PS Claim 2; Page 74; 115pp; English.
XX
CC This sequence represents a cassava vein mosaic virus promoter, and
CC is a nucleic acid molecule of the invention. The promoter is capable of
CC initiating transcription of an operably linked heterologous nucleic acid
CC sequence in a plant cell. The CSMV promoters are active in both monocot
CC and dicot plant species, and therefore can be readily applied to a
CC variety of cultivated crops. Although generally constitutive, the
CC derivative promoters include promoters that can regulate expression in a
CC tissue-specific manner, and therefore are useful for controlling
CC expression of heterologous genes in a tissue-specific manner. The
CC promoters can be used for producing transgenic plants with an altered
CC phenotype.
XX
SQ Sequence 392 BP; 154 A; 64 C; 83 G; 91 T; 0 other;

Query Match 20.1%; Score 120.6; DB 19; Length 392;
Best Local Similarity 93.3%; Pred. No. 6.2e-27;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGACGTAAAGCACTGACGACACATGTAAGAAAGACATTAAGTCGTGAT 152
DB 143 GAATCTTGAAGACGTAAAGCACTGACGACACATGTAAGAAAGACATTAAGTCGTGAT 202
QY 153 TGTGAAGAGACATGAGGACATGTAAGGTAAGGTAAGGCGGAAAGTAACTT 212
DB 203 TGTGAAGAGACATGAGGACATGTAAGGTAAGGTAAGGCGGAAAGTAACTT 262
QY 213 ATGCAATTTGTAATTT 227
DB 263 ATCACAAGGAATCT 277

RESULT 14
AAV14021
ID AAV14021 standard; DNA; 411 BP.
XX
AC AAV14021;
XX
DT 18-JUN-1998 (first entry)
XX
DE CSMV promoter pB.
XX
KM Cassava vein mosaic virus; CSMV; promoter; cultivated crop;
KM tissue-specific expression control; transgenic plant; ss.
XX
OS Cassava vein mosaic virus.
XX
PN WO9748819-A1.
XX
PD 24-DEC-1997.
XX
PF 20-JUN-1997; 97WO-US10376.
XX
PR 20-JUN-1996; 96US-0020129.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Beachy RN, De Kochko A, Fauquet C, Verdagner B;
XX
DR WPI; 1998-063157/06.
XX
PT Cassava vein mosaic virus promoter - used to express heterologous
PT DNA sequences for producing transgenic plants having altered
PT phenotype(s)

XX Claim 2; Page 76-77; 115pp: English.
PS
XX This sequence represents a cassava vein mosaic virus promoter, and
CC is a nucleic acid molecule of the invention. The promoter is capable of
CC initiating transcription of an operably linked heterologous nucleic acid
CC sequence in a plant cell. The CaMV promoters are active in both monocot
CC and dicot plant species, and therefore can be readily applied to a
CC variety of cultivated crops. Although generally constitutive, the
CC derivative promoters include promoters that can regulate expression in a
CC tissue-specific manner, and therefore are useful for controlling
CC expression of heterologous genes in a tissue-specific manner. The
CC promoters can be used for producing transgenic plants with an altered
CC phenotype.
XX
SQ Sequence 411 BP; 157 A; 60 C; 87 G; 107 T; 0 other;
Query Match 20.1%; Score 120.6; DB 19; Length 411;
Best Local Similarity 93.3%; Pred. No. 6.3e-27;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 93 GAATATTGACGTAAGCACTGACGACACATGAAAAGAAAGATAGGTGCGTAT 152
DB 107 GAATCTTGAAGACGTAAGCACTGACGACACATGAAAAGAAAGATAGGTGCGTAT 166
QY 153 TGTGAAGAGACATAGAGGACACATGTAAGGTGGAATGTAAGGCGGAAAGTAACTT 212
DB 167 TGTGAAGAGACATAGAGGACACATGTAAGGTGGAATGTAAGGCGGAAAGTAACTT 226
QY 213 ATGCATTGTAAATT 227
DB 227 ATCACAAGGAATCT 241

RESULT 15
ID AAA96836
AC AAA96836;
DT 19-FEB-2001 (first entry)
DE Promoter from intergenic region of Cassava vein mosaic virus.
KW Promoter; intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; ss.
XX
OS Cassava vein mosaic virus.
XX
PN W0200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI: 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
PS Claim 4; Page 80; 91pp: English.
XX
CC The present sequence represents a promoter fragment from the intergenic

CC region of Cassava vein mosaic virus. The promoter is used to construct
CC chimeric expression promoters. These chimeric promoters comprise a
CC nucleic acid sequence which is derived from a first plant promoter,
CC in which a plant vascular expression promoter region is replaced with
CC a nucleic acid sequence derived from a second plant promoter comprising
CC a plant green tissue expression promoter region. Preferably, the first
CC plant promoter originates from commelina yellow mottle virus, and the
CC second plant promoter originates from the Cassava vein mosaic virus.
CC The chimeric promoters are useful for producing transgenic plants.
XX
SQ Sequence 515 BP; 198 A; 79 C; 109 G; 129 T; 0 other;
Query Match 20.1%; Score 120.6; DB 21; Length 515;
Best Local Similarity 93.3%; Pred. No. 6.9e-27;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 93 GAATATTGACGTAAGCACTGACGACACATGAAAAGAAAGATAGGTGCGTAT 152
DB 216 GAATCTTGAAGACGTAAGCACTGACGACACATGAAAAGAAAGATAGGTGCGTAT 275
QY 153 TGTGAAGAGACATAGAGGACACATGTAAGGTGGAATGTAAGGCGGAAAGTAACTT 212
DB 276 TGTGAAGAGACATAGAGGACACATGTAAGGTGGAATGTAAGGCGGAAAGTAACTT 335
QY 213 ATGCATTGTAAATT 227
DB 336 ATCACAAGGAATCT 350

Search completed: April 14, 2003, 08:19:41
Job time : 196.814 secs

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:01:47 ; Search time 61.8557 Seconds
(without alignments)
2974.765 Million cell updates/sec

Title: US-09-963-803-22

Perfect score: 600

Sequence: 1 aagcttgctgcctgcagca.....cacacaactagagatcc 600

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/1/lna/5B COMB.seq:*
3: /cgn2_6/ptodata/1/lna/5A COMB.seq:*
4: /cgn2_6/ptodata/1/lna/5B COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCTUS COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfileseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	54.8	9.1	7218	1	US-08-232-463-14 Sequence 14, Appl
2	40.4	6.7	439	1	US-08-247-809A-3 Sequence 3, Appl
3	40.4	6.7	439	2	US-08-711-728-3 Sequence 3, Appl
4	40.4	6.7	446	1	US-08-764-100-23 Sequence 23, Appl
5	40.4	6.7	532	3	US-09-042-426-1 Sequence 1, Appl
6	40.4	6.7	532	3	US-09-291-238-1 Sequence 1, Appl
7	40.4	6.7	532	4	US-09-330-760-1 Sequence 1, Appl
8	40.4	6.7	532	4	US-09-328-473-1 Sequence 1, Appl
9	40.4	6.7	532	4	US-09-330-737-1 Sequence 1, Appl
10	40.4	6.7	532	4	US-09-329-169-1 Sequence 1, Appl
11	40.4	6.7	532	4	US-09-330-714A-1 Sequence 1, Appl
12	40.4	6.7	532	4	US-09-328-826-1 Sequence 1, Appl
13	40.4	6.7	560	3	US-09-042-426-5 Sequence 5, Appl
14	40.4	6.7	560	4	US-09-291-238-5 Sequence 5, Appl
15	40.4	6.7	560	4	US-09-330-760-5 Sequence 5, Appl
16	40.4	6.7	560	4	US-09-328-473-5 Sequence 5, Appl
17	40.4	6.7	560	4	US-09-330-737-5 Sequence 5, Appl
18	40.4	6.7	560	4	US-09-329-169-5 Sequence 5, Appl
19	40.4	6.7	560	4	US-09-330-714A-5 Sequence 5, Appl
20	40.4	6.7	560	4	US-09-328-826-5 Sequence 5, Appl
21	40.4	6.7	661	4	US-09-027-998A-33 Sequence 33, Appl
22	40.4	6.7	793	4	US-08-371-764-1 Sequence 1, Appl
23	40.4	6.7	793	4	US-08-897-736-1 Sequence 1, Appl
24	40.4	6.7	831	1	US-08-450-834-5 Patent No. 5177308
25	40.4	6.7	950	6	5177308-3 Patent No. 5177308
26	40.4	6.7	978	1	US-08-446-486-31 Sequence 31, Appl
27	40.4	6.7	978	1	US-08-463-308-31 Sequence 31, Appl

28	40.4	6.7	979	1	US-08-446-486-30 Sequence 30, Appl
29	40.4	6.7	979	1	US-08-463-308-30 Patent No. 5254799
30	40.4	6.7	980	6	5254799-30 Sequence 46, Appl
31	40.4	6.7	1030	1	US-07-936-163-46 Sequence 43, Appl
32	40.4	6.7	1030	4	US-08-729-601A-43 Sequence 35, Appl
33	40.4	6.7	1034	4	US-09-363-970-35 Sequence 8, Appl
34	40.4	6.7	1138	4	US-09-011-151-8 Sequence 9, Appl
35	40.4	6.7	1138	4	US-09-011-151-9 Sequence 46, Appl
36	40.4	6.7	1196	4	US-08-729-601A-46 Sequence 2, Appl
C 37	40.4	6.7	1279	4	US-09-185-244-2 Sequence 6, Appl
C 38	40.4	6.7	1279	4	US-09-471-913-6 Sequence 2, Appl
C 39	40.4	6.7	1303	3	US-08-894-440-2 Sequence 2, Appl
40	40.4	6.7	1303	4	US-09-458-093-2 Sequence 5, Appl
41	40.4	6.7	1651	3	US-09-065-999-5 Sequence 6, Appl
42	40.4	6.7	1651	3	US-09-065-999-6 Sequence 5, Appl
43	40.4	6.7	1722	1	US-08-247-809A-5 Sequence 5, Appl
44	40.4	6.7	1722	2	US-08-711-728-5 Sequence 17, Appl
45	40.4	6.7	1829	1	US-07-966-187-17

ALIGNMENTS

RESULT 1
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINER, F.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)836-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZ9PT-F15
; US-08-232-463-14
Query Match 9.1% Score 54.8; DB 1; Length 7218;

US-08-764-100-23
: Sequence 23, Application US/08764100
: Patent No. 5773700
: GENERAL INFORMATION:
: APPLICANT: van Grinsven J., Martinus Q.
: APPLICANT: De Haan, Petrus T.
: APPLICANT: Gielen L., Johannes J.
: APPLICANT: Peters, Dirk
: APPLICANT: Goldbach, Robert W.
: TITLE OF INVENTION: Improvements in or Relating to Organic
: NUMBER OF INVENTION: Compounds
: CORRESPONDENCE ADDRESSES: 27
: ADDRESSEE: Sandoz Agro, Inc
: STREET: 975 California Avenue
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/764,100
: FILING DATE: 06-DEC-1996
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/214,064
: FILING DATE:
: APPLICATION NUMBER: US 08/032,235
: FILING DATE: 17-MAR-1993
: APPLICATION NUMBER: GB 9206016.9
: FILING DATE: 19-MAR-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5773700r1s, Allen E.
: REGISTRATION NUMBER: 34,490
: REFERENCE/DOCKET NUMBER: 137-1061
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 354-3592
: TELEFAX: (415) 857-1125
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 446 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-764-100-23

Query Match 6.7%; Score 40.4; DB 1; Length 446;
Best Local Similarity 88.0%; Pred. No. 0.0028;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ZIP: 07901
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/042,426
: FILING DATE: March 13, 1998
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoxie, Thomas
: REGISTRATION NUMBER: 32,993
: REFERENCE/DOCKET NUMBER: 135/1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8614
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 532 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: IMMEDIATE SOURCE:
: CLONE: 35S Promoter
: US-09-042-426-1

Query Match 6.7%; Score 40.4; DB 3; Length 532;
Best Local Similarity 88.0%; Pred. No. 0.003;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

US-09-291-238-1
: Sequence 1, Application US/09291238
: Patent No. 6222104
: GENERAL INFORMATION:
: APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
: TITLE OF INVENTION: DNA Construct Containing Bacillus
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: No. 6222104artis Corporation
: STREET: 564 Morris Avenue
: CITY: Summit
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07901
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/291,238
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/042,426
: FILING DATE: March 13, 1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoxie, Thomas
: REGISTRATION NUMBER: 32,993
: REFERENCE/DOCKET NUMBER: 135/1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8614
: TELEFAX: (919) 541-8689

;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 532 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
;; IMMEDIATE SOURCE:
US-09-291-238-1

Query Match 6.7%; Score 40.4; DB 4; Length 532;
Best Local Similarity 88.0%; Pred. No. 0.003;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 327 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 376
DB 274 GATTGATGATATCTCCACTGACGTAAAGGATGACGACAAATCCACTA 323

RESULT 7

US-09-330-760-1
; Sequence 1, Application US/09330760
; Patent No. 6229075
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6229075artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,760
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,426
; FILING DATE: March 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
US-09-330-760-1

Query Match 6.7%; Score 40.4; DB 4; Length 532;
Best Local Similarity 88.0%; Pred. No. 0.003;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 327 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 376
DB 274 GATTGATGATATCTCCACTGACGTAAAGGATGACGACAAATCCACTA 323

RESULT 8

US-09-328-473-1
; Sequence 1, Application US/09328473
; Patent No. 6232533
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6232534artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,473
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,426
; FILING DATE: March 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
US-09-328-473-1

Query Match 6.7%; Score 40.4; DB 4; Length 532;
Best Local Similarity 88.0%; Pred. No. 0.003;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 327 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 376
DB 274 GATTGATGATATCTCCACTGACGTAAAGGATGACGACAAATCCACTA 323

RESULT 9

US-09-330-737-1
; Sequence 1, Application US/09330737
; Patent No. 6232534
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6232534artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit

STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,737
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: Match 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-330-737-1

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 4; Length 532;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 327 GATTGATGATATCTCCACTGACGTAAAGGATGACCGACGACTA 376
|||||
274 GATTGATGATATCTCCACTGACGTAAAGGATGACCGACGACTA 323

RESULT 10
US-09-329-169-1
Sequence 1, Application US/09329169
Patent No. 6329575
GENERAL INFORMATION:
APPLICANT: Irvn J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6329575artis Corporation
STREET: 564 Morris Avenue
City: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,169
FILING DATE: 09-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas

REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-329-169-1

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 4; Length 532;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 327 GATTGATGATATCTCCACTGACGTAAAGGATGACCGACGACTA 376
|||||
274 GATTGATGATATCTCCACTGACGTAAAGGATGACCGACGACTA 323

RESULT 11
US-09-330-714A-1
Sequence 1, Application US/09330714A
Patent No. 6342660
GENERAL INFORMATION:
APPLICANT: Irvn J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6342660artis Corporation
STREET: 564 Morris Avenue
City: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,714A
FILING DATE: 11-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:

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; CLONE: 35S Promoter
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-330-714A-1

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 4; Length 532;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 327 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGACTA 376
DB 274 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGACTA 323

RESULT 12
US-09-328-826-1
; Sequence 1, Application US/09328826
; Patent No. 6399860
; GENERAL INFORMATION:
; APPLICANT: Irvln J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6399860artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,826
; FILING DATE: 09-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,426
; FILING DATE: March 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-328-826-1

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 4; Length 532;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
; Patent No. 6114608
; GENERAL INFORMATION:
; APPLICANT: Irvln J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6114608artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,426
; FILING DATE: March 13, 1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
US-09-042-426-5

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 3; Length 560;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 327 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGACTA 376
DB 322 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGACTA 371

RESULT 14
US-09-291-238-5
; Sequence 5, Application US/09291238
; Patent No. 6222104
; GENERAL INFORMATION:
; APPLICANT: Irvln J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6222104artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/291,238
; FILING DATE:
```

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,426
; FILING DATE: March 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
; US-09-291-238-5

Query Match          6.7%; Score 40.4; DB 4; Length 560;
Best Local Similarity 88.0%; Pred. No. 0.0031;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY  327 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 376
      |||||||||||||||||||||||||||||||||||||||
Db   322 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 371

RESULT 15
US-09-330-760-5
; Sequence 5, Application US/09330760
; Patent No. 6229075
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6229075artis Corporation
; STREET: 564 Morris Avenue
; City: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,760
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,426
; FILING DATE: March 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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```

; MOLECULE TYPE: DNA (genomic)
; HYPOTHEtical: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
; US-09-330-760-5

Query Match          6.7%; Score 40.4; DB 4; Length 560;
Best Local Similarity 88.0%; Pred. No. 0.0031;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY  327 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 376
      |||||||||||||||||||||||||||||||||||||||
Db   322 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 371

Search completed: April 14, 2003, 10:28:42
Job time : 67.8557 secs
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Db 121 AACATGAAAGAGAAAGTAAGTGGGTGATGTGTAAGAGACATAGAGACACATGTA 180
Qy 181 AGGTGAAAATGTAAGGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTACT 240
Db 181 AGGTGAAAATGTAAGGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTACT 240
Qy 241 GATTGATGATATCAAGATTGATGATATCTCCAGCTAGCAAGGATGACGCTGCG 300
Db 241 GATTGATGATATCAAGATTGATGATATCTCCAGCTAGCAAGGATGACGCTGCG 300
Qy 301 ACGACTAGTATGATGATATCAAGATTGATGATATCTCCAGCTAGCAAGGATG 360
Db 301 ACGACTAGTATGATGATATCAAGATTGATGATATCTCCAGCTAGCAAGGATG 360
Qy 361 ACGCATGCCAGCACTAGTATGATGATATCAAGATTGATGATATCTCCAGCTAG 420
Db 361 ACGCATGCCAGCACTAGTATGATGATATCAAGATTGATGATATCTCCAGCTAG 420
Qy 421 TAAGGATGACGATGCCAGCACTAGTATGATGATATCAAGATTGATGATATCT 480
Db 421 TAAGGATGACGATGCCAGCACTAGTATGATGATATCAAGATTGATGATATCT 480
Qy 481 CCAGTACGCTAAGGATGACGATGCCAGCTTACCGGTATGCCGTTCCAAAGCTTAT 540
Db 481 CCAGTACGCTAAGGATGACGATGCCAGCTTACCGGTATGCCGTTCCAAAGCTTAT 540
Qy 541 TTCCTATTATTAAGCACTTGTAGTACTTAGAAAACCAACAACTAGAGATCC 600
Db 541 TTCCTATTATTAAGCACTTGTAGTACTTAGAAAACCAACAACTAGAGATCC 600
```

RESULT 2

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US-09-963-803-20
; Sequence 20, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963, 803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1163
; NAME/KEY: promoter
; LOCATION: (1)..(462)
; OTHER INFORMATION:
US-09-963-803-20
```

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Query Match 62.3%; Score 373.6; DB 9; Length 462;
Best Local Similarity 95.3%; Pred. No. 2e-102;
Matches 385; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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Qy 1 AAGCTTGCAATGCGTGCAGACTAGTATCCGCGTCATCAATGACATACACAGTCTGA 60
Db 1 AAGCTTGCAATGCGTGCAGACTAGTATCCGCGTCATCAATGACATACACAGTCTGA 60
Qy 61 GGAGATGATTAAGTACGATGACACTGCTGCGAATATTGAAGAGCTAAGACACTGACG 120
Db 61 GGAGATGATTAAGTACGATGACACTGCTGCGAATATTGAAGAGCTAAGACACTGACG 120
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Qy 121 AACATGAAAGAGAAAGTAAGTGGGTGATGTGTAAGAGACATAGAGACACATGTA 180
Db 121 AACATGAAAGAGAAAGTAAGTGGGTGATGTGTAAGAGACATAGAGACACATGTA 180
Qy 181 AGGTGAAAATGTAAGGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTACT 240
Db 181 AGGTGAAAATGTAAGGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTACT 240
Qy 241 GATTGATGATATCAAGATTGATGATATCTCCAGCTAGCAAGGATGACGCTGCG 300
Db 241 GATTGATGATATCAAGATTGATGATATCTCCAGCTAGCAAGGATGACGCTGCG 300
Qy 301 ACGACTAGTATGATGATATCAAGATTGATGATATCTCCAGCTAGCAAGGATG 360
Db 301 ACGACTAGTATGATGATATCAAGATTGATGATATCTCCAGCTAGCAAGGATG 360
Qy 361 ACGCATGCCAGCACTAGTATGATGATATCAAGATTGATGATATCTCCAGCTAG 404
Db 361 ACGCATGCCAGCACTAGTATGATGATATCAAGATTGATGATATCTCCAGCTAG 404
```

RESULT 3

```
US-09-963-803-23
; Sequence 23, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963, 803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1167
; NAME/KEY: promoter
; LOCATION: (1)..(604)
; OTHER INFORMATION:
US-09-963-803-23
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Query Match 52.0%; Score 312.2; DB 9; Length 604;
Best Local Similarity 84.5%; Pred. No. 6.1e-84;
Matches 442; Conservative 0; Mismatches 3; Indels 78; Gaps 5;
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Qy 78 CATGACACTCTGTGCGAATATTGAAGAGCTGAAGCACTGACCAACAATGAAAAGAA 137
Db 160 CATGCCACTCTGTGCGAATATTGAAGAGCTGAAGCACTGACCAACAATGAAAAGAA 219
Qy 138 GATTAAGTGGGATTTGTAAGAGACATAGAGGACACATGTAAGTGGAAAATGTAAG 197
Db 220 GATTAAGTGGGATTTGTAAGAGACATAGAGGACACATGTAAGTGGAAAATGTAAG 278
Qy 198 GCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGTATGATGATATCA 257
Db 279 GCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGTATGATGATATCA 314
Qy 258 GATTGATGATATCTCCAGCTAGCAAGGATGACGATGCCAGCTAGTATGATG 317
Db 315 -----CTAGTATGATG 327
Qy 318 TGATATCAAGATTGATGATATCTCCAGCTAGCAAGGATGACGATGCCAGCTAG 377
Db 328 TGATATCAAGATTGATGATATCTCCAGCTAGCAAGGATGACGATGCCAGCTAG 385
```


;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: PCT IB00/00370
;; PRIOR FILING DATE: 2000-10-05
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 21
;; LENGTH: 392
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: promoter MP11164
;; NAME/KEY: promoter
;; LOCATION: (1)..(392)
;; OTHER INFORMATION:
US-09-963-803-21

Query Match 39.0%; Score 234.2; DB 9; Length 392;
Best Local Similarity 96.8%; Pred. No. 1.3e-60;
Matches 239; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 AAGCTTGATGCGCTGACACTAGTATCCGCGTCATCAATGACATCATCAGTACTGA 60
DB 1 AAGCTTGATGCGCTGACACTAGTATCCGCGTCATCAATGACATCATCAGTACTGA 60
OY 61 GGAGATGATAGTACCTGACCTGACCTCTGTGCGAATATTGAAGACGTAAAGCAGCAG 120
DB 61 GGAGATGATAGTACCTGACCTGACCTCTGTGCGAATATTGAAGACGTAAAGCAGCAG 120
OY 121 AACATGAAAAGAAAGTAAGTTCGCGTATGTAAGAAAGACATAGAGACATATGA 180
DB 121 AACATGAAAAGAAAGTAAGTTCGCGTATGTAAGAAAGACATAGAGACATATGA 180
OY 181 AGGTGAAAATGTAAAGGCGGAAAGTAACCTTATGCAATTTGTAATTTGGTTACGACTAGT 240
DB 181 AGGTGAAAATGTAAAGGCGGAAAGTAACCTTATGCAATTTGTAATTTGGTTACGACTAGT 240
OY 241 GATTGAT 247
DB 241 GCGTCAT 247

RESULT 7
US-09-963-803-3
; Sequence 3, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow n
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 317
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Promoter MP11116
;; NAME/KEY: promoter
;; LOCATION: (1)..(317)
;; OTHER INFORMATION:
US-09-963-803-3

Query Match 35.4%; Score 212.4; DB 9; Length 317;
Best Local Similarity 99.5%; Pred. No. 4e-54;

Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 20 ACTAGTATCCGCGTCATCATGACATCATCATGACTAGTGAAGATGATAGCTAGCA 79
DB 18 ACTAGTATCCGCGTCATCATGACATCATCATGACTAGTGAAGATGATAGCTAGCA 77
OY 80 TGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTAAAGACAAATGAAAAGAAAGA 139
DB 78 TGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTAAAGACAAATGAAAAGAAAGA 137
OY 140 TAAGTCGCTGATTTGTGAAGACATAGAGACATAGTAAAGTGGAAAATGTAAGGCC 199
DB 138 TAAGTCGCTGATTTGTGAAGACATAGAGACATAGTAAAGTGGAAAATGTAAGGCC 197
OY 200 GAAAGTAACCTTATGCAATTTGTAATTTGTTAC 233
DB 198 GAAAGTAACCTTATGCAATTTGTAATTTGTTAC 231

RESULT 8
US-09-963-803-25
; Sequence 25, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 25
;; LENGTH: 472
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: promoter MP11169
;; NAME/KEY: promoter
;; LOCATION: (1)..(472)
;; OTHER INFORMATION:
US-09-963-803-25

Query Match 35.4%; Score 212.4; DB 9; Length 472;
Best Local Similarity 91.5%; Pred. No. 4.9e-54;
Matches 236; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

OY 78 CATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTAAAGACAAATGAAAAGAAAGA 137
DB 160 CATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTAAAGACAAATGAAAAGAAAGA 219
OY 138 GATGAGTCGCGTATTTGTAAGACATAGAGACATGATTAAGTGAAGTGAAGTGAAG 197
DB 220 GATGAGTCGCGTATTTGTAAGACATAGAGACATGATTAAGTGAAGTGAAGTGAAG 278
OY 198 GCGGAAAGTAACCTTATGCAATTTGTAATTTGTTACGATAGATGATGATGATGATCA 257
DB 279 GCGGAAAGTAACCTTATGCAATTTGTAATTTGTTACGATAGATGATGATGATGATCA 338
OY 258 GATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 317
DB 339 GATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 398
OY 318 TGATATCAAGATTTGATG 335
DB 399 GGTTCCTCAAGCTTTATTTT 416

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RESULT 9
US-09-963-803-4
; Sequence 4, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963.803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPR1117
; NAME/KEY: promoter
; LOCATION: (1)..(348)
; OTHER INFORMATION:
US-09-963-803-4

Query Match          33.4%; Score 200.4; DB 9; Length 348;
Best Local Similarity 99.1%; Pred. No. 1.7e-50;
Matches 212; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 20 ACTGATCCCGCTCATCATGACATCATCATGAGAGATGATGCTAGCCA 79
    |||||||
DB 52 ACTGATCCCGCTCATCATGACATCATCATGAGAGATGATGCTAGCCA 111
    |||||||
QY 80 TGACACTCTGTGCAATATTGAAGACATGACACTGACGACAAATGAAAGAAAGA 139
    |||||||
DB 112 TGACACTCTGTGCAATATTGAAGACATGACACTGACGACAAATGAAAGAAAGA 171
    |||||||
QY 140 TAAGTCGGTGATTTGTGAAGACATGAGACACATGTAAGTGGAAATGTAAGGCC 199
    |||||||
DB 172 TAAGTCGGTGATTTGTG -AAGAGACATGAGACACATGTAAGTGGAAATGTAAGGCC 230
    |||||||
QY 200 GGAAGTAACTTATGCAATTGTAATTGGTTAC 233
    |||||||
DB 231 GGAAGTAACTTATGCAATTGTAATTGGTTAC 264
    |||||||

RESULT 10
US-09-963-803-5
; Sequence 5, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963.803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPR1146
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; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(371)
; OTHER INFORMATION:
US-09-963-803-5

Query Match          25.5%; Score 152.8; DB 9; Length 371;
Best Local Similarity 98.1%; Pred. No. 3.4e-36;
Matches 154; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 78 CATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAATGAAAGAGAA 137
    |||
DB 130 CATGCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAATGAAAGAGAA 189
    |||
QY 138 GATAAGTCGGTGATTTGTGAAGACATGAGACACATGTAAGTGGAAATGTAAGG 197
    |||
DB 190 GATAAGTCGGTGATTTGTGAAGACATGAGACACATGTAAGTGGAAATGTAAGG 249
    |||
QY 198 GCGGAAGTAACTTATGCAATTGTAATTGGTTAC 233
    |||
DB 250 GCGGAAGTAACTTATGCAATTGTAATTGGTTAC 285
    |||

RESULT 11
US-09-963-803-7
; Sequence 7, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yell
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963.803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPR1154
; NAME/KEY: promoter
; LOCATION: (1)..(301)
; OTHER INFORMATION:
US-09-963-803-7

Query Match          23.5%; Score 140.8; DB 9; Length 301;
Best Local Similarity 98.1%; Pred. No. 1.2e-32;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 78 CATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAATGAAAGAGAA 137
    |||
DB 63 CATGCCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAATGAAAGAGAA 122
    |||
QY 138 GATAAGTCGGTGATTTGTGAAGACATGAGACACATGTAAGTGGAAATGTAAGG 197
    |||
DB 123 GATAAGTCGGTGATTTGTG -AAGAGACATGAGACACATGTAAGTGGAAATGTAAGG 181
    |||
QY 198 GCGGAAGTAACTTATGCAATTGTAATTGGTTAC 233
    |||
DB 182 GCGGAAGTAACTTATGCAATTGTAATTGGTTAC 217
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RESULT 12
US-09-963-803-6
; Sequence 6, Application US/09963803
; Publication No. US20030028922A1
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? GENERAL INFORMATION:
? APPLICANT: Meristem Therapeutics
? TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow fl
? TITLE OF INVENTION: virus and cassava vein mosaic virus
? FILE REFERENCE: 184332042
? CURRENT APPLICATION NUMBER: US/09/963,803
? PRIORITY FILING DATE: 2001-09-26
? PRIOR APPLICATION NUMBER: FR 99/03925
? PRIOR FILING DATE: 1999-03-29
? PRIOR APPLICATION NUMBER: PCT IB00/00370
? PRIOR FILING DATE: 2000-10-05
? NUMBER OF SEQ ID NOS: 39
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 6
? LENGTH: 398
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: promoter MP1147
? FEATURE:
? NAME/KEY: promoter
? LOCATION: (1)..(398)
? OTHER INFORMATION:
? US-09-963-803-6

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Query Match	23.5%	Score 140.8;	DB 9;	Length 398;
Best Local Similarity	98.1%	Pred. No. 1.4e-32;		
Matches 153; Conservative	0;	Mismatches 2;	Indels 1;	Gaps 1;

Qy	78	CATGACACTCTGTCCGAATATTGGAAGCGTAGACACAGACAAACAATGAAAGAA	137
Db	160	CATGCCACTCTGTGCGAATATTGGAAGCGTAGACACAGACAAACAATGAAAGAA	219
Qy	138	GATTAAGTGGCGGTGATTTGTGAAAGAGACATAGAGACACATGTAAGTGGGAAAATGT	197
Db	220	GATTAAGTGGCGGTGATTTGTG -AAGGAGACATAGAGACACATGTAAGTGGGAAAATGT	278
Qy	198	GCGGAAGTAACCTTATGCATTTGTGTAATTTGGTTAC	233
Db	279	GCGGAAGTAACCTTATGCATTTGTGTAACCTTGGTTAC	314

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RESULT 13
US-09-963-803-2
Sequence 2, Application US/09963803
Publication NO. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: vitruis and cassava vein mosaic virus
FILE REFERENCE: 164332042
CURRENT APPLICATION NUMBER: US/09/963, 803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 515
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter from the intergenic region of Cassava Vein Mosaic virus
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(515)
OTHER INFORMATION:
US-09-963-803-2

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Query Match	20.18;	Score 120.6;	DB 9;	Length 515;
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	Best Local Similarity	93.3%	Pred. No. 1.8e-26	Matches 126	Conservative 0	Mismatches 9	Indels 0	Gaps 0
OY	93	GAATTTTGAAGACGCTAACACCTGACGACACAACAAATGAAAAGAAAGATTAAGTCGGTGT	152					
Db	216	GAATCTTTGAAACGCTAACACCTGACGACACAACATATAAAGAAAGATTAAGTCGGTGT	275					
OY	153	TGTTGAAGACGACATTAAGGCGGAAAGTAAACCTT	212					
Db	276	TGTTGAAGACGACATTAAGGCGGAAAGTAAACCTT	335					
OY	213	ATTCATTTGTAATTTT	227					
Db	336	ATTCACCAAGAACTT	350					

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RESULT 14
US-09-765-555-1
? Sequence 1, Application US/09765555
? Publication No. US20030037355A1
? GENERAL INFORMATION:
? APPLICANT: The Scripps Research Institute
? TITLE OF INVENTION: Methods and compositions to modulate
? TITLE OF INVENTION: expression in plants
? FILE REFERENCE: 27801-20014.40
? CURRENT APPLICATION NUMBER: US/09/765,555
? CURRENT FILING DATE: 2002-05-24
? PRIOR APPLICATION NUMBER: US 09/620,897
? PRIOR FILING DATE: 2000-01-21
? PRIOR APPLICATION NUMBER: US 60/177,468
? PRIOR FILING DATE: 2000-01-21
? NUMBER OF SEQ ID NOS: 75
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1
? LENGTH: 532
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Promoter CasvMV
US-09-765-555-1

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Query Match      20.1%: Score 120.6; DB: 9; Length 532;
Best Local Similarity 93.3%: Pred. No. 1, Be-26;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      93  GAATATTGAGACGCTAAGCACTGACGACACACAAATGAAAAGAAAGAAATAGGTGCGTGAT 152
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       231  GAATCTTGAAGACGCTAAGCACTGACGACACAAATGAAAAGAAAGAAATAGGTGCGTGAT 290

QY      153  TGTGAAGAGACATAGAGGACATGTAAAGTGGAAAAATGTAAAGGGCGAAAGTAACCTT 212
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       291  TGTGAAGAGACATAGAGGACATGTAAAGTGGAAAAATGTAAAGGGCGAAAGTAACCTT 350

QY      213  ATGCATTTGTAATT 227
          || || || || |
Db       351  ATCACAAAAGCAATCT 365

RESULT 15
US-09-847-057-4/C
: Sequence 4, Application US/09847057
: Patent No. US20020004943A1
: GENERAL INFORMATION:
: APPLICANT: AGRINOMICS, LLC.
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN P
: FILE REFERENCE: PAGODA
: CURRENT APPLICATION NUMBER: US/09/847,057
: CURRENT FILING DATE: 2001-05-01
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: Patentin version 3.0
: SEQ ID NO 4
: LENGTH: 8340
: TYPE: DNA

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Tue Apr 15 15:12:21 2003

us-09-963-803-22.rnpb

Page 7

ORGANISM: Binary vector pAG14002
US-09-847-057-4

Query Match	20.1%	Score 120.6;	DB 10;	Length 8340;
Best Local Similarity	93.3%	Pred. NO. 6.9e-26;		
Matches 126; Conservative	0;	Mismatches 9;	Indels 0;	Gaps 0;

QY	93	GAATATTTGAAGACGTAGACACCTGACGACAAACATGAAAGAAGAAATTAAGCTCGCTAT	152
Db	7853	GAATCTTTGAAGACGTAAAGCCTGACGACAAACATGAAAGAAGAAATTAAGCTCGCTAT	7794
QY	153	TGTTAAAGACACATAGACGACACATGTAAGGTGGAAATGTAAAGGGCGGAAAGTAACCTT	212
Db	7793	TGTGAAAGACACATAGAGGACACACATGTAAGGTGGAAATGTAAAGGGCGGAAAGTAACCTT	7734
QY	213	ATGCATTTGTAATTT	227
Db	7733	ATCACAAGGAATCT	7719

Search completed: April 14, 2003, 12:29:12
Job time : 76.1649 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:13:29 ; Search time 2420.62 Seconds

(without alignments)
6232.082 Million cell updates/sec

Title: US-09-963-803-22

Perfect score: 600

Sequence: 1 aagcttgcatgcctgcagca.....cacacacactagagatcc 600

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3	312.2	52.0	604	36	US-09-963-803-23				Sequence 23, Appl		
4	304.6	50.8	393	36	US-09-963-803-19				Sequence 19, Appl		
5	281.4	46.9	341	36	US-09-963-803-24				Sequence 24, Appl		
6	234.2	39.0	392	36	US-09-963-803-21				Sequence 21, Appl		
7	212.4	35.4	317	36	US-09-963-803-3				Sequence 3, Appl		
8	212.4	35.4	472	36	US-09-963-803-25				Sequence 25, Appl		
9	200.4	33.4	348	36	US-09-963-803-2				Sequence 4, Appl		
10	152.8	25.5	371	36	US-09-963-803-5				Sequence 5, Appl		
11	140.8	23.5	301	36	US-09-963-803-7				Sequence 7, Appl		
12	140.8	23.5	398	36	US-09-963-803-6				Sequence 6, Appl		
13	120.6	20.1	392	1	PCT-US97-10376-1				Sequence 1, Appl		
14	120.6	20.1	392	1	PCT-US97-10376A-1				Sequence 1, Appl		
15	120.6	20.1	392	16	US-09-202-838A-1				Sequence 1, Appl		
16	120.6	20.1	392	16	US-09-202-838B-1				Sequence 1, Appl		
17	120.6	20.1	411	1	PCT-US97-10376-4				Sequence 4, Appl		
18	120.6	20.1	411	1	PCT-US97-10376A-4				Sequence 4, Appl		
19	120.6	20.1	411	16	US-09-202-838A-4				Sequence 4, Appl		
20	120.6	20.1	411	16	US-09-202-838B-4				Sequence 4, Appl		
21	120.6	20.1	515	25	US-09-641-466-1				Sequence 1, Appl		

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29 120.6 20.1 526 1 PCT-US97-10376-3 Sequence 3, Appl1
30 120.6 20.1 532 30 PCT-US97-10376A-3 Sequence 3, Appl1
31 120.6 20.1 532 30 US-09-673-274A-19 Sequence 19, Appl1
32 120.6 20.1 838 26 US-09-673-274A-19 Sequence 2, Appl1
33 120.6 20.1 853 25 US-09-641-466-2 Sequence 20, Appl1
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35 120.6 20.1 8340 32 US-09-874-057-4 Sequence 4, Appl1
36 120.6 20.1 8340 33 PCT-US01-50638-5 Sequence 5, Appl1
37 120.6 20.1 12241 35 US-09-948-138-4 Sequence 4, Appl1
38 120.6 20.1 12241 35 US-10-033-190-5 Sequence 5, Appl1
39 120.6 20.1 12241 38 US-10-033-190-5 Sequence 5, Appl1
40 117.4 19.6 305 1 PCT-US97-10376-5 Sequence 5, Appl1
41 117.4 19.6 305 1 PCT-US97-10376A-5 Sequence 5, Appl1
42 117.4 19.6 305 16 US-09-202-838-5 Sequence 5, Appl1
43 117.4 19.6 305 16 US-09-202-838A-5 Sequence 9, Appl1
44 117.4 19.6 420 1 PCT-US97-10376-9 Sequence 9, Appl1
45 117.4 19.6 420 1 PCT-US97-10376A-9 Sequence 9, Appl1
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ALIGNMENTS

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RESULT 1
US-09-963-803-22
; Sequence 22, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter Mpr1165
; NAME/KEY: promoter
; LOCATION: (1)..(600)
; OTHER INFORMATION:
US-09-963-803-22
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Best Local Similarity 100.0%; Pred. No. 8,9e-163;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GGAGATGAATAGCTAGCCCTGACACTCTGTGGCAATATTGAAGAGCTAAGCACTGACGAC 120
QY 121 AACCAATGAAGAAGAGAAAGTAAGTGGTATTGTGAAGAAGACATAGAGACACATGTA 180
DB 121 AACCAATGAAGAAGAGAAAGTAAGTGGTATTGTGAAGAAGACATAGAGACACATGTA 180
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QY 181 AGGTGGAANAATGTAAAGCGCGGAAGTAACCTTATGCAATTTGTAATTTGCTACGACTACT 240
DB 181 AGGTGGAANAATGTAAAGCGCGGAAGTAACCTTATGCAATTTGTAATTTGCTACGACTACT 240
QY 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTACGTAAGGATGACGATGCC 300
DB 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTACGTAAGGATGACGATGCC 300
QY 301 ACAGTACGATGATGATATATCAAGATTGATGTGATATCTCCACTACGTAAGGATG 360
DB 301 ACAGTACGATGATGATATATCAAGATTGATGTGATATCTCCACTACGTAAGGATG 360
QY 361 ACAGTACGATGATGATATATCAAGATTGATGTGATATCTCCACTACGTAAGGATG 420
DB 361 ACAGTACGATGATGATATATCAAGATTGATGTGATATCTCCACTACGTAAGGATG 420
QY 421 TAAGGATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 TAAGGATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 CCACGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 CCACGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 TTCCCTTATTTAAAGCACTTGTGTAGTACTTAAAGCAACACACACACACACCTAGAGATCC 600
DB 541 TTCCCTTATTTAAAGCACTTGTGTAGTACTTAAAGCAACACACACACACACCTAGAGATCC 600
```

```
RESULT 2
US-09-963-803-20
; Sequence 20, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter Mpr1163
; NAME/KEY: promoter
; LOCATION: (1)..(462)
; OTHER INFORMATION:
US-09-963-803-20
```

```
Query Match 62.3%; Score 373.6; DB 36; Length 462;
Best Local Similarity 95.3%; Pred. No. 2,9e-97;
Matches 385; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
```

```
QY 1 AAGCTTGCACTGCTGCAGACACTAGTATCGCGCGTCATCATGACATCATCAGTACTGA 60
DB 1 AAGCTTGCACTGCTGCAGACACTAGTATCGCGCGTCATCATGACATCATCAGTACTGA 60
QY 61 GGAGATGAATAGCTAGCCCTGACACTCTGTGGCAATATTGAAGAGCTAAGCACTGACGAC 120
DB 61 GGAGATGAATAGCTAGCCCTGACACTCTGTGGCAATATTGAAGAGCTAAGCACTGACGAC 120
QY 121 AACCAATGAAGAAGAGAAAGTAAGTGGTATTGTGAAGAAGACATAGAGACACATGTA 180
DB 121 AACCAATGAAGAAGAGAAAGTAAGTGGTATTGTGAAGAAGACATAGAGACACATGTA 180
```


Query Match	52.0%	Score 312.2	DB 36	Length 604
Best Local Similarity	84.5%	Pred. No. 1.9e-79		
Matches 442	Conservative	0	Mismatches 3	Indels 78
				Gaps 5
QY 78	CATGCACTCTGTGGGATATTGAAGACGTAAACACTGCACCAACATGAAGAAGAA	137		
DB 160	CATGCCACTCTGTGGGATATTGAAGACGTAAACACTGCACCAACATGAAGAAGAA	219		
QY 138	GATAAGTCGGTGTGATTGTGAAAAGACACATAGAGCACATGTAAAGTGGAAATGTAA	197		
DB 220	GATAAGTCGGTGTGATTGTGAAAAGACACATAGAGCACATGTAAAGTGGAAATGTAA	278		
QY 198	GGCGAAATTAACCTTATGCATTTTGAATTTGGTTACGCACTAGTGATTGATGTATCAA	257		
DB 279	GGCGAAATTAACCTTATGCATTTTGAATTTGGTTAC-----	314		
QY 258	GATTGATGTGATTCACCTCAGTAAAGGATGAACGATGCCACAGACTAGTATGATG	317		
DB 315	-----CTAGTGATGTGATG	327		
QY 318	TGATATCAAGATTGTGATGATATCTCCACTGACGTAAAGGATGAGCATGCCACGACTAG	377		
DB 328	TGATATCAAGATTGTGATGATATCTCCACTGACGTAAAGGATGAGCATGCCAC--CTAG	385		
QY 378	TGATTGATGTATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGAGCATGC	437		
DB 386	TGATTGATGTATATCAAGATTGATGTATATCTCCACTGACGTAAAGGATGAGCATGC	445		

Query Match	Similarity	50.8%	Score 304.6	DB 36	Length 393
Best Local	Similarity	94.3%	Pred. No. 2.6e-77		
Matches 316	Conservative	0	Mismatches 19	Indels	Gaps
QY 1	AAGCTTGATGCTCTCACCACACTAGATATCGCGCGTATCATATGACATCATACAGTACTGA	60			
Db 1	AAGCTTGCATGCGCTGCAGACACTAGATATCGCGCGTATCATATGACATCATACAGTACTGA	60			
QY 61	GGAGTATGAATAGCTATGCCATGACACTCTCTGTGGAAATATTGAAGACGTAGCACTGACGC	120			
Db 61	GGAGTATGAATAGCTATGCCATGACACTCTGTGGAAATATTGAAGACGTAGCACTGACGC	120			
QY 121	AACAATGAAAAGACAGAATAGTACGTGGTGTATTGTGAAGAGACATAGAGACACATGTA	180			
Db 121	AACATGTAAAAGACAAAATATAGTTCGGTGATTTGAAAAGACACATAGAGACACATGTA	180			
QY 181	AGGTGAAAATGTATAGGGGGGAAAGATAACCTATGATTTGTAAATTTGATTTCGACTACT	240			
Db 181	AGGTGAAAATGTATAGGGGGGAAAGATAACCTATGATTTGTAAATTTGATTTCGACTACT	240			
QY 241	GATTGATGTGATATACAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCC	300			
Db 241	GATTGATGTGATATACAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCC	300			
QY 301	ACGACTAGTATGATGTGATATCAAGATGTATGTT 335				
Db 301	ACGTTACCCGGTATGCCGGTTGCCAAGCTTTATTTT 335				

RESULT 5

US-09-963-803-24

: Sequence 24, Application US/09963803

```

; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1168
; NAME/KEY: promoter
; LOCATION: (1)..(541)
; OTHER INFORMATION:
US-09-963-803-24
```

```

Query Match          46.9%; Score 281.4; DB 36; Length 541;
Best Local Similarity 93.3%; Pred. No. 1,5e-70;
Matches 305; Conservative 0; Mismatches 21; Indels 1; Gaps 1;
```

```

QY 78 CATGACACTCTGCGCAATATGAGACCTAAGCACTGACGACACATGAATGAAGAAAGAA 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 160 CATGCCACTGTGCGAAATATGAGACCTAAGCACTGACGACACATGAATGAAGAAAGAA 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 138 GATAAGCTGCGTATGTTGAAAGACATAGAGACACATGTAAGTGGAAATGTAAGG 197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 220 GATTAAGCTGGTGATGTGTC-AAGAGACATAGAGACACATGTAAGTGGAAATGTAAGG 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 198 GCGGAAAGTAACCTTATGCAATTGTGTAATTTGTTACGACTAGTATGATGATATCAA 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 279 GCGGAAAGTAACCTTATGCAATTGTGTAATTTGTTACGACTAGTATGATGATATCAA 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 258 GATTGATGATATCTCCACTGACGTAGAGGATGACGATGCCAGCACTAGTATGATGATG 317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 339 GATTGATGATATCTCCACTGACGTAGAGGATGACGATGCCAGCACTAGTATGATGATG 398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 318 TGATATCAAGATGATGATATCTCCACTGACGTAGAGGATGACGATGCCAGCACTAG 377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 399 TGATATCAAGATGATGATATCTCCACTGACGTAGAGGATGACGATGCCAGCACTAG 458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 378 TGATTGATGATATCAAGATGATGAT 404
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 459 CGGTATGCTGTGCCCAACCTTATTT 485
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

RESULT 6
US-09-963-803-21
; Sequence 21, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 392
; TYPE: DNA
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1164
; NAME/KEY: promoter
; LOCATION: (1)..(392)
; OTHER INFORMATION:
US-09-963-803-21
```

```

Query Match          39.0%; Score 234.2; DB 36; Length 392;
Best Local Similarity 96.8%; Pred. No. 6,3e-57;
Matches 239; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```

QY 1 AAGCTTGATGCTGCGACACTAGTATCCGCCGTCATCAATGACATCATCAGTACTGA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 AAGCTTGATGCTGCGACACTAGTATCCGCCGTCATCAATGACATCATCAGTACTGA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GGAGATGAATAGTACGCTGACACTGTGCGAATATTGAAGACGTAAAGCACTAGCAGC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 GGAGATGAATAGTACGCTGACACTGTGCGAATATTGAAGACGTAAAGCACTAGCAGC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 AACATGAAAGAGAGATAGTGTGCGTATGTAAGACATAGAGACATGACATGTA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 AACATGAAAGAGAGATAGTGTGCGTATGTAAGACATAGAGACATGACATGTA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 AGGTGGAATATGTAAGGCGGGAAGTAACCTTATGCAATTTGTAATTTGGTTACGACTAGT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 AGGTGGAATATGTAAGGCGGGAAGTAACCTTATGCAATTTGTAATTTGGTTACGACTAGT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 GATTGAT 247
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 GCGTCAT 247
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

RESULT 7
US-09-963-803-3
; Sequence 3, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 317
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr116
; NAME/KEY: promoter
; LOCATION: (1)..(317)
; OTHER INFORMATION:
US-09-963-803-3
```

```

Query Match          35.4%; Score 212.4; DB 36; Length 317;
Best Local Similarity 99.5%; Pred. No. 1,2e-50;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 20 ACTAGTATCCGCCGTCATCATGACATCATCACTAGTACGAGAGATGATGATGCA 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 18 ACTAGTATCCGCCGTCATCATGACATCATCACTAGTACGAGAGATGATGATGCA 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 TGACACTGTGTCGATATTTGAAGACGTAAAGCACTGACGACACAACATGAAAGAGAGA 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 78 TGACACTGTGTCGATATTTGAAGACGTAAAGCACTGACGACACAACATGAAAGAGAGA 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

RESULT 9
US-09-963-803-4
: Sequence 4, Application US/09963803
: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow r
: TITLE OF INVENTION: virus and cassava vein mosaic virus
: FILE REFERENCE: 184332042
: CURRENT APPLICATION NUMBER: US/09/963,803
: CURRENT FILING DATE: 2001-09-26

```

Query Match	25.5%;	Score 152.8;	DB 36;	Length 371;
Best Local Similarity	98.7%;	Pred. 1.2.3e-33;		
Matches 154;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;
0y	78	CATGCACTCTGTGGCATATTGGAAGACGTAAAGCACTGCACGACACATGAAAGAGAA	137	

Db 130 CATGCCACTCTGTGCGAATATTGGAAGACGTAAAGCACTGACGACACAAATGAAAAGAAGAA 189
 Qy 138 GATAAGTGGTGATTTGTGAAGAAGACATAGAGACATGTAAGGTGAAAAATGTAAG 197
 Db 190 GATAAGTGGTGATTTGTGAAGAAGACATAGAGACACATGTAAGGTGAAAAATGTAAG 249
 Qy 198 GCGGAAAGTAACCTTATGCAATTTGTAATTTGGTTAC 233
 Db 250 GCGGAAAGTAACCTTATGCAATTTGTAATTTGGTTAC 285

RESULT 11

US-09-963-803-7
 ; Sequence 7, Application US/09963803
 ; GENERAL INFORMATION:
 ; APPLICANT: Meristem Therapeutics
 ; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
 ; FILE REFERENCE: 184332042
 ; CURRENT APPLICATION NUMBER: US/09/963,803
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: FR 99/03925
 ; PRIOR FILING DATE: 1999-03-29
 ; PRIOR APPLICATION NUMBER: PCT IB00/00370
 ; PRIOR FILING DATE: 2000-10-05
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 301
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: promoter MPr1154
 ; NAME/KEY: promoter
 ; LOCATION: (1)..(301)
 ; OTHER INFORMATION:
 US-09-963-803-7

Query Match

Best Local Similarity 98.1%; Score 140.8; DB 36; Length 301;
 Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 78 CATGACACTCTGTGCGAATATTGGAAGACGTAAAGCACTGACGACACAAATGAAAAGAAGAA 137
 Db 63 CATGCCACTCTGTGCGAATATTGGAAGACGTAAAGCACTGACGACACAAATGAAAAGAAGAA 122
 Qy 138 GATAAGTGGTGATTTGTGAAGAAGACATAGAGACATGTAAGGTGAAAAATGTAAG 197
 Db 123 GATAAGTGGTGATTTGTG-AAGAGACATAGAGACATGTAAGGTGAAAAATGTAAG 181
 Qy 198 GCGGAAAGTAACCTTATGCAATTTGTAATTTGGTTAC 233
 Db 182 GCGGAAAGTAACCTTATGCAATTTGTAATTTGGTTAC 217

RESULT 12

US-09-963-803-6
 ; Sequence 6, Application US/09963803
 ; GENERAL INFORMATION:
 ; APPLICANT: Meristem Therapeutics
 ; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
 ; FILE REFERENCE: 184332042
 ; CURRENT APPLICATION NUMBER: US/09/963,803
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: FR 99/03925
 ; PRIOR FILING DATE: 1999-03-29
 ; PRIOR APPLICATION NUMBER: PCT IB00/00370
 ; PRIOR FILING DATE: 2000-10-05
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6

; LENGTH: 398
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: promoter MPr1147
 ; NAME/KEY: promoter
 ; LOCATION: (1)..(398)
 ; OTHER INFORMATION:
 US-09-963-803-6

Query Match

Best Local Similarity 98.1%; Score 140.8; DB 36; Length 398;
 Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 78 CATGACACTCTGTGCGAATATTGGAAGACGTAAAGCACTGACGACACAAATGAAAAGAAGAA 137
 Db 160 CATGCCACTCTGTGCGAATATTGGAAGACGTAAAGCACTGACGACACAAATGAAAAGAAGAA 219
 Qy 138 GATAAGTGGTGATTTGTGAAGAAGACATAGAGACACATGTAAGGTGAAAAATGTAAG 197
 Db 220 GATAAGTGGTGATTTGTG-AAGAGACATAGAGACACATGTAAGGTGAAAAATGTAAG 278
 Qy 198 GCGGAAAGTAACCTTATGCAATTTGTAATTTGGTTAC 233
 Db 279 GCGGAAAGTAACCTTATGCAATTTGTAATTTGGTTAC 314

RESULT 13

PCT-US97-10376-1
 ; Sequence 1, Application PC/TUS9710376
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: CASSAVA VEIN MOSAIC VIRUS PROMOTERS AND
 ; NUMBER OF SEQUENCES: 36
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 20-JUN-1997
 ; APPLICATION NUMBER: PCT/US97/10376
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/020,129
 ; FILING DATE: 20-JUN-1996
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 392 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; PCT-US97-10376-1

Query Match

Best Local Similarity 93.3%; Score 120.6; DB 1; Length 392;
 Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 93 GATATTGGAAGACGTAAAGCACTGAGACAAATGAAAAGAAGATTAAGTGGTGAT 152
 Db 143 GATCTTGAAGACGTAAAGCACTGAGACAAATGAAAAGAAGATTAAGTGGTGAT 202
 Qy 153 TGTGAAGACATAGAGACACATGTAAGGTGAAAATGTAAGGCGGAAAGTAACCTT 212
 Db 203 TGTGAAGACATAGAGACACATGTAAGGTGAAAATGTAAGGCGGAAAGTAACCTT 262
 Qy 213 ATGCATTTGTAATTT 227

Db 263 ATCACAAAGAAATCT 277

RESULT 14

PCT-US97-10376A-1

; Sequence 1, Application PC/TUS97/10376A

; GENERAL INFORMATION:

; APPLICANT: Verdaguer, Bertrand

; APPLICANT: de Kochko, Alexandre

; APPLICANT: Beachy, Roger N.

; APPLICANT: Fauquet, Claude

; TITLE OF INVENTION: CASSAVA VEIN MOSAIC VIRUS PROMOTERS AND

; TITLE OF INVENTION: USES THEREOF

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE

; STREET: 10550 North Torrey Pines Road

; CITY: La Jolla

; STATE: California

; COUNTRY: US

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/10376A

; FILING DATE: 20-JUN-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/020,129

; FILING DATE: 20-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; REFERENCE/DOCKET NUMBER: 504.1PC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 784-2937

; TELEFAX: (619) 784-9399

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 392 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; PCT-US97-10376A-1

Query Match 20.1%; Score 120.6; DB 1; Length 392;

Best Local Similarity 93.3%; Pred. No. 4.9e-24;

Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATTTGAAGACGTAAGCACTGACGACACATGAAAAAGAGATAGTGGTGTAT 152

DB 143 GAATCTTGAAGACGTAAGCACTGACGACACATGAAAAAGAGATAGTGGTGTAT 202

QY 153 TGTGAAGAGACATGAGAGACATGTAAGTGAATAATGTAAGGCGGAAAGTAACCTT 212

DB 203 TGTGAAGAGACATGAGAGACATGTAAGTGAATAATGTAAGGCGGAAAGTAACCTT 262

QY 213 ATGCAATTGTATTT 227

DB 263 ATCACAAAGAAATCT 277

RESULT 15

US-09-202-838-1

; Sequence 1, Application US/09202838

; GENERAL INFORMATION:

; APPLICANT: Verdaguer, Bertrand

; APPLICANT: de Kochko, Alexandre

; APPLICANT: Beachy, Roger N.

; APPLICANT: Fauquet, Claude

; TITLE OF INVENTION: CASSAVA VEIN MOSAIC VIRUS PROMOTERS AND USES THEREOF

; FILE REFERENCE: MYC00115

; CURRENT APPLICATION NUMBER: US/09/202,838

; CURRENT FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: PCT/US97/10376

; PRIOR FILING DATE: 1997-06-20

; PRIOR APPLICATION NUMBER: 60/020,129

; PRIOR FILING DATE: 1996-06-20

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: Patentln Ver. 2.1

; SEQ ID NO 1

; LENGTH: 392

; TYPE: DNA

; ORGANISM: Cassava vein mosaic virus

US-09-202-838-1

Query Match 20.1%; Score 120.6; DB 16; Length 392;

Best Local Similarity 93.3%; Pred. No. 4.9e-24;

Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATTTGAAGACGTAAGCACTGACGACACATGAAAAAGAGATAGTGGTGTAT 152

DB 143 GAATCTTGAAGACGTAAGCACTGACGACACATGAAAAAGAGATAGTGGTGTAT 202

QY 153 TGTGAAGAGACATGAGAGACATGTAAGTGAATAATGTAAGGCGGAAAGTAACCTT 212

DB 203 TGTGAAGAGACATGAGAGACATGTAAGTGAATAATGTAAGGCGGAAAGTAACCTT 262

QY 213 ATGCAATTGTATTT 227

DB 263 ATCACAAAGAAATCT 277

Search completed: April 14, 2003, 12:06:34

Job time : 2423.62 secs

Qy	93	GAATATATGAGACGTAGACATGCGACCAACATGAAACAAAGAAAGTAAGTGGCGAT	122
Db	231	GAATCTTGAAGACGTAAAGCACTGACGACCAACATGAAACAAAGAAAGTAAGTGGCGAT	230
Qy	153	TGTGAAAGAACACATAGGAGACACATCTTAAGCTGAAATATTAAGGCGGAGAAATACCTT	212
Db	291	TGTGAAAGAACACATAGGAGACACATGTAAAGGTGAAATATTAAGGCGGAGAAATACCTT	350
Qy	213	ATGCATTGTGAATTT	227
Db	351	ATCACAAAGGAATCT	365

```

: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic oligonucleotide
: FEATURE:
: NAME/KEY: promoter
: LOCATION: (7)...(532)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (539)...(736)
: FEATURE:
: NAME/KEY: terminator
: LOCATION: (767)...(1030)
US-09-673-274B-20

Query Match      20.1%  Score 120.6;  DB 6;  Length 1036;
Best Local Similarity 93.3%  Pred. No. 1.9e-25;
Matches 126;  Conservative 0;  Mismatches 9;  Indels 0;  Gaps 0;

OY      93  GAATTTTGAAGACGTAAACACTGACGACACAACTAATAAAGAAGATTAAGTCGTCGAT 152
      ||| |||||
DB      222  GAATTTTGAAGACGTAAACACTGACGACACAACTAATAAAGAAGATTAAGTCGTCGAT 281
      ||| |||||

OY      153  TGTGAAAGAGACATTAAGAGACACATGTAAGGTGAAAAATGTAAGGCGGAAAGTAACCTT 212
      |||||
DB      282  TGTGAAAGAGACATTAAGAGACACATGTAAGGTGAAAAATGTAAGGCGGAAAGTAACCTT 341
      |||||

OY      213  ATGCATTTGTAATTT 227
      || |||||
DB      342  ATCACAANGAGTCT 356

RESULT 4
US-10-380-935-30
: Sequence 30, Application US/10380935
: GENERAL INFORMATION:
: APPLICANT: WARNER, Simon, Anthony, James
: APPLICANT: HAWKES, Timothy, Robert
: APPLICANT: ANDREWS, Christopher, John
: TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
: FILE REFERENCE: PPD50594/MO
: CURRENT APPLICATION NUMBER: US/10/380,935
: PRIOR FILING DATE: 2003-03-19
: PRIOR APPLICATION NUMBER: GB0023911.1
: PRIOR FILING DATE: 2000-09-29
: PRIOR APPLICATION NUMBER: GB0027693.1
: PRIOR FILING DATE: 2000-11-13
: PRIOR APPLICATION NUMBER: GB0023910.3
: PRIOR FILING DATE: 2000-09-29
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 30
: LENGTH: 309
: TYPE: DNA
: ORGANISM: Cauliflower Mosaic Virus
: FEATURE:
: OTHER INFORMATION: Enhancer
US-10-380-935-30

Query Match      6.7%  Score 40.4;  DB 8;  Length 309;
Best Local Similarity 88.0%  Pred. No. 0.073;
Matches 44;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;

OY      336  GATTGATGTGATATCTCCACATGACGTAAAGGATGACGATGCCAGACTA 445
      |||||
DB      242  GATTGATGTGATATCTCCACATGACGTAAAGGATGACGACAAATCCACTA 291
      |||||

RESULT 5
US-10-380-935-37
: Sequence 37, Application US/10380935
: GENERAL INFORMATION:
: APPLICANT: WARNER, Simon, Anthony, James
: APPLICANT: HAWKES, Timothy, Robert

```



```
; APPLICANT: ANDREWS, Christopher, John
; TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: PPD50594/MO
; CURRENT APPLICATION NUMBER: US/10/380,935
; PRIOR FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: GB0023911.1
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: GB0027693.1
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: GB0023910.3
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Pigwort Mosaic Virus
; FEATURE:
; OTHER INFORMATION: Enhancer
US-10-380-935-37

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 8; Length 522;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTGATATCTCCACTGAGCGATGAGGATGCGCATGCCAGCACTA 445
DB 459 GATTGATGTGATATCTCCACTGAGCGATGAGGATGAGGATGAGCAACATCCCACTA 508

RESULT 6
US-10-391-414-10
; Sequence 10, Application US/10391414
; GENERAL INFORMATION:
; APPLICANT: SHINOZAKI, Kazuko
; APPLICANT: KATSURA, Koji
; APPLICANT: ITO, Yusuke
; TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
; FILE REFERENCE: 382.1041
; CURRENT APPLICATION NUMBER: US/10/391,414
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: JP 2002-377316
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 835
; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-10-391-414-10

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 8; Length 835;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGAGCGATGAGGATGCGCATGCCAGCACTA 307
DB 729 GATTGATGTGATATCTCCACTGAGCGATGAGGATGAGGATGAGCAACATCCCACTA 778

RESULT 7
US-60-434-166-147
; Sequence 147, Application US/60434166
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology
; APPLICANT: Creelman, Robert A.
; APPLICANT: Haake, Volker
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Adam, Luc J.
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Riechmann, Jose Luis
```

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; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0051 P
; CURRENT APPLICATION NUMBER: US/60/434,166
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 559
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G2227
US-60-434-166-147

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 11; Length 1683;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGAGCGATGAGGATGCGCATGCCAGCACTA 307
DB 9 GATTGATGTGATATCTCCACTGAGCGATGAGGATGAGGATGAGCAACATCCCACTA 58

RESULT 8
US-10-302-267-1
; Sequence 1, Application US/10302267
; GENERAL INFORMATION:
; APPLICANT: Keddle, James
; APPLICANT: Fromm, Michael
; APPLICANT: Heard, Jacqueline
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc
; APPLICANT: Biron, Pierie
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, Lynne
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Creelman, Robert
; TITLE OF INVENTION: PLANT GENE SEQUENCES II
; FILE REFERENCE: MBI-0007
; CURRENT APPLICATION NUMBER: US/10/302,267
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US/09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/120,880
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/121,037
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 60/124,278
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: 60/129,450
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/135,134
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/144,153
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/161,143
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/162,656
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2361
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144)..(2024)
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```
; OTHER INFORMATION: G274
US-10-302-267-1

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 2361;
Best Local Similarity 88.0%; Pred. No. 0.13;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTATATCTCCACTGACGTAAGGATGATGATGCCAGCACTA 307
      |||
DB 113 GATTGATGTATATCTCCACTGACGTAAGGATGATGATGCCAGCACTA 162

RESULT 9
US-10-130-150-13
; Sequence 13, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein
US-10-130-150-13

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 3212;
Best Local Similarity 88.0%; Pred. No. 0.15;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTATATCTCCACTGACGTAAGGATGATGATGCCAGCACTA 307
      |||
DB 197 GATTGATGTATATCTCCACTGACGTAAGGATGATGATGCCAGCACTA 246

RESULT 10
US-10-130-150-18
; Sequence 18, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein fused
; OTHER INFORMATION: and ER retaining signal peptides
US-10-130-150-18

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 3288;
Best Local Similarity 88.0%; Pred. No. 0.15;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTATATCTCCACTGACGTAAGGATGATGATGCCAGCACTA 307
      |||
DB 197 GATTGATGTATATCTCCACTGACGTAAGGATGATGATGCCAGCACTA 246

RESULT 11
US-10-130-150-15
; Sequence 15, Application US/10130150
; GENERAL INFORMATION:

; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 3329
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein fuse
; OTHER INFORMATION: signal peptide
US-10-130-150-15

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 3329;
Best Local Similarity 88.0%; Pred. No. 0.15;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTATATCTCCACTGACGTAAGGATGATGATGCCAGCACTA 307
      |||
DB 197 GATTGATGTATATCTCCACTGACGTAAGGATGATGATGCCAGCACTA 246

RESULT 12
US-10-160-764-40
; Sequence 40, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailifoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: In Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 5247
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; OTHER INFORMATION: PB1121-35S-AtPFA
US-10-160-764-40

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 5247;
Best Local Similarity 88.0%; Pred. No. 0.17;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTATATCTCCACTGACGTAAGGATGATGATGCCAGCACTA 307
      |||
DB 3209 GATTGATGTATATCTCCACTGACGTAAGGATGATGATGCCAGCACTA 3258

RESULT 13
US-10-160-764-4
; Sequence 4, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailifoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
```

```
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5250
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-4

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 5250;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCGATGCCAGACTA 307
Db 3209 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCGACATCCCACTA 3258

RESULT 14
US-10-160-764-48
; Sequence 48, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailloux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 5511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-48

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 5511;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCGATGCCAGACTA 307
Db 3209 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCGACATCCCACTA 3258

RESULT 15
US-10-160-764-52
; Sequence 52, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailloux, Maryse
; APPLICANT: Wang, Yang
```

```
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; APPLICANT: Chailloux, Maryse
; APPLICANT: Wang, Yang
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 5715
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-52

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 5715;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCGATGCCAGACTA 307
Db 3209 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCGACATCCCACTA 3258

Search completed: April 14, 2003, 12:27:55
Job time : 490.052 secs
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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 06:53:52 ; Search time 1394.64 Seconds
(without alignments)
6967.603 Million cell updates/sec

Title: US-09-963-803-22

Perfect score: 600
Sequence: 1 aagcttgcatgcctgcagca.....cacacacactagagatcc 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43.8	7.3	224	17	BH746858
2	42.4	7.1	561	13	BH162517
3	41.8	7.0	1101	17	CNS00396
4	41	6.8	222	13	BH161725
5	40.4	6.7	112	17	BH751161
6	40.4	6.7	142	17	BH749349

Result No.	Score	Query Match	Length	DB ID	Description
7	40.4	6.7	153	17	BH619283
8	40.4	6.7	158	17	BH747013
9	40.4	6.7	153	17	BH748291
10	40.4	6.7	165	17	BH747357
11	40.4	6.7	175	17	BH746616
12	40.4	6.7	177	17	BH802465
13	40.4	6.7	190	17	BH752801
14	40.4	6.7	193	17	BH748289
15	40.4	6.7	214	17	BH747829
16	40.4	6.7	215	17	BH753813
17	40.4	6.7	219	17	BH747744
18	40.4	6.7	220	17	BH747438
19	40.4	6.7	221	17	BH802415
20	40.4	6.7	230	17	BH746474
21	40.4	6.7	230	17	BH799173
22	40.4	6.7	237	17	BH802463
23	40.4	6.7	244	17	BH746375
24	40.4	6.7	248	17	BH254798
25	40.4	6.7	251	17	BH750171
26	40.4	6.7	254	17	BH748500
27	40.4	6.7	256	17	BH748499
28	40.4	6.7	258	17	BH802470
29	40.4	6.7	261	17	BH802493
30	40.4	6.7	268	17	BH611919
31	40.4	6.7	269	17	BH211646
32	40.4	6.7	269	17	BH802489
33	40.4	6.7	271	17	BH799178
34	40.4	6.7	272	17	BH802428
35	40.4	6.7	274	17	BH802495
36	40.4	6.7	279	17	BH748475
37	40.4	6.7	281	17	BH750170
38	40.4	6.7	281	17	BH802443
39	40.4	6.7	284	17	BH213307
40	40.4	6.7	284	17	BH746665
41	40.4	6.7	286	17	BH747007
42	40.4	6.7	293	17	BH610310
43	40.4	6.7	296	17	BH213532
44	40.4	6.7	335	17	BH213230
45	40.4	6.7	344	17	BH747662

ALIGNMENTS

RESULT 1
BH746858
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BH746858 224 bp DNA linear GSS 27-FEB-2002
SALK_003694.51.40.x Arabidopsis thaliana genomic clone SALK_003694.51.40.x, DNA
Arabidopsis thaliana genomic clone SALK_003694.51.40.x, DNA
sequence.
BH746858
BH746858.1 GI:18959973
GSS.
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 224)
Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,
'C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Predans,L., Shinn,P.,
'Zimmerman,J., and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis genome
unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of

termini were treated with pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size fractionated DNA was then separated on a 1% agarose

ORIGIN	Query Match	Score	DB	Length
NC_000962.1	6.7%	40.4	17	112

Matches 44: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGATATCTCCACGTAGGATGAGCATGCGACAGACTA 445
 |||||||||||||||||||||||||||||||||||||||
 Db 3 GATTGATGATATCTCCACGTAGGATGAGCATGCGACACTCACTA 52

RESULT 6
 LOCUS BH749349 142 bp DNA linear GSS 27-FEB-2002
 DEFINITION SALK_047736.48.15.x Arabidopsis thaliana TDNA insertion lines
 sequence.
 Arabidopsis thaliana genomic clone SALK_047736.48.15.x, DNA
 accession
 BH749349
 VERSION BH749349.1 GI:18964144
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 142)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J., and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckere@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1..142
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_047736.48.15.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 41 a 36 c 30 g 35 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 142;
 Best Local Similarity 88.0%; Pred. No. 3;
 Matches 44: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGATATCTCCACGTAGGATGAGCATGCGACAGACTA 445
 |||||||||||||||||||||||||||||||||||||||
 Db 33 GATTGATGATATCTCCACGTAGGATGAGCATGCGACACTCACTA 82

RESULT 7
 LOCUS BH619283 153 bp DNA linear GSS 30-JAN-2002
 DEFINITION SALK_040762 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_040762, DNA sequence.
 accession
 BH619283
 VERSION BH619283.1 GI:18429799
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 153)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J., and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
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 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckere@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1..153
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_040762"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 36 a 34 c 36 g 47 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 153;
 Best Local Similarity 88.0%; Pred. No. 3;
 Matches 44: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGATATCTCCACGTAGGATGAGCATGCGACAGACTA 445
 |||||||||||||||||||||||||||||||||||||||
 Db 110 GATTGATGATATCTCCACGTAGGATGAGCATGCGACACTCACTA 61

RESULT 8
 LOCUS BH747013 153 bp DNA linear GSS 27-FEB-2002
 DEFINITION SALK_008070.43.05.x Arabidopsis thaliana TDNA insertion lines
 sequence.
 Arabidopsis thaliana genomic clone SALK_008070.43.05.x, DNA
 accession
 BH747013
 VERSION BH747013.1 GI:18960128
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 153)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J., and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
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 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckere@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

FEATURES Location/Qualifiers

SOURCE

1. 153

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_008070.43.05.x"

/note="1kb-Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

BASE COUNT 47 a 37 c 33 g 36 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 153;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 445
|||||
Db 44 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 93

RESULT 9
BH748291 158 bp DNA linear GSS 27-FEB-2002
LOCUS SALK_045100.51.10.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_045100.51.10.x, DNA
sequence.
ACCESSION BH748291
VERSION BH748291.1 GI:18961648
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 158;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 445
|||||
Db 110 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 61

RESULT 10
BH747357 165 bp DNA linear GSS 27-FEB-2002
LOCUS SALK_016522.55.50.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_016522.55.50.x, DNA
sequence.
ACCESSION BH747357
VERSION BH747357.1 GI:18960472
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 165;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 445
|||||
Db 34 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 83

REFERENCE
AUTHORS Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
, C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckers@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. 165
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_016522.55.50.x"
/note="1kb-Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 165;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 445
|||||
Db 34 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 83

REFERENCE
AUTHORS Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
, C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Contact: Joseph R. Ecker
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10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckers@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. 158
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_045100.51.10.x"
/note="1kb-Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 165;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 445
|||||
Db 34 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 83

REFERENCE
AUTHORS Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
, C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Contact: Joseph R. Ecker
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10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckers@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. 158
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_045100.51.10.x"
/note="1kb-Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 165;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 445
|||||
Db 34 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 83

FEATURES Location/Qualifiers

SOURCE

1. 158

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_045100.51.10.x"

/note="1kb-Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

BASE COUNT 37 a 35 c 37 g 49 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 165;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 445
|||||
Db 34 GATTGATGTGATATCTCCACTGACGTAGGATGACGATGCCAGCACTA 83

ACCESSION BH746616 GI:18959731
 VERSION BH746616.1
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
 Spermatophyta; Magnoliophyta: eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 175)
 REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadlinab,
 C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J., and Ecker,J.R.
 A Sequence-indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 JOURNAL Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckere@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 CLASS: TDNA tagged.
 FEATURES
 source
 Location/Qualifiers
 1..175
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_045268.54.50.x"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at <http://signal.salk.edu/tdna-protocols.html>"
 BASE COUNT 54 a 43 c 40 g 38 t
 ORIGIN
 Query Match 6.7%; Score 40.4; DB 17; Length 175;
 Best Local Similarity 88.0%; Pred. No. 3;
 Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 396 GATTGATGATATCTCCACTGACGTAAAGGATGACGATCCACGACTA 445
 |||||||||||||||||||||||||||||||||||
 Db 66 GATTGATGATATCTCCACTGACGTAAAGGATGACGATCCACGACTA 115
 RESULT 12
 BH802465 177 bp DNA linear GSS 25-APR-2002
 LOCUS 1008026610.y2 1008 - Rescuemu Grid I Zea mays genomic, DNA
 DEFINITION
 sequence.
 ACCESSION BH802465
 VERSION BH802465.1 GI:20316614
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 177)
 REFERENCE Walbot,V.
 Maize genomic sequences found using engineered Rescuemu transposon
 unpublished (2001)
 JOURNAL Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221

Email: walbot@stanford.edu
 Very probable ligation site found so sequence was trimmed.
 Post-ligation sequence submitted separately.
 Plate: 1008026 row: 10
 Class: transposon tagged.
 FEATURES
 source
 Location/Qualifiers
 1..177
 /organism="Zea mays"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /clone="lib-1008 - Rescuemu Grid I"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: leaf; Vector: Rescuemu (engineered from
 pluescript backbone); Site_1: BamHI; Site_2: BglII;
 Rescuemu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on Rescuemu, go to the web
 site www.zmmb.jastate.edu and follow the links for
 'Rescuemu.' Grid I was grown at Berkeley in 2001. DNA was
 extracted from leaf punches, double digested using BamHI
 and BglII, and ligated to form circular plasmids. DH10B
 cells were transformed and then screened on LB plates with
 ampicillin."
 BASE COUNT 39 a 38 c 47 g 53 t
 ORIGIN
 Query Match 6.7%; Score 40.4; DB 17; Length 177;
 Best Local Similarity 88.0%; Pred. No. 3;
 Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 327 GATTGATGATATCTCCACTGACGTAAAGGATGACGATCCACGACTA 376.
 |||||||||||||||||||||||||||||||||||
 Db 118 GATTGATGATATCTCCACTGACGTAAAGGATGACGATCCACGACTA 69
 RESULT 13
 BH752801 190 bp DNA linear GSS 27-FEB-2002
 LOCUS SALK_019366.54.25.x Arabidopsis thaliana TDNA insertion lines
 DEFINITION Arabidopsis thaliana genomic clone SALK_019366.54.25.x, DNA
 sequence.
 ACCESSION BH752801
 VERSION BH752801.1 GI:18972023
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
 Spermatophyta; Magnoliophyta: eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 190)
 REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadlinab,
 C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J., and Ecker,J.R.
 A Sequence-indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 JOURNAL Contact: Joseph R. Ecker
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 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckere@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 CLASS: TDNA tagged.
 FEATURES
 source
 Location/Qualifiers
 1..190
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"

/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 52 a 52 c 41 g 45 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 190;
Best Local Similarity 88.0%; Pred. No. 3.1;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 396 GATTGATGATATCTCCACTGACGTAAAGGATGACCATCCACGACTA 445
|||||
DB 81 GATTGATGATATCTCCACTGACGTAAAGGATGACCATCCACGACTA 130
|||||

RESULT 14
BH748289 193 bp DNA linear GSS 27-FEB-2002
LOCUS SALK_045097.54.25.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_045097.54.25.x, DNA
sequence.
ACCESSION BH748289
VERSION BH748289.1 GI:18961643
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 193)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadri nab
, C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J. and Ecker,J.R.
A Sequence-indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
CONTACT: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. 193
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 61 a 48 c 43 g 41 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 193;
Best Local Similarity 88.0%; Pred. No. 3.1;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 396 GATTGATGATATCTCCACTGACGTAAAGGATGACCATCCACGACTA 445

|||||
DB 84 GATTGATGATATCTCCACTGACGTAAAGGATGACCATCCACGACTA 133
|||||

RESULT 15
BH747829 214 bp DNA linear GSS 27-FEB-2002
LOCUS SALK_035354.55.75.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_035354.55.75.x, DNA
sequence.
ACCESSION BH747829
VERSION BH747829.1 GI:18960944
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 214)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadri nab
, C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J. and Ecker,J.R.
A Sequence-indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
CONTACT: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. 214
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 58 a 56 c 52 g 48 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 214;
Best Local Similarity 88.0%; Pred. No. 3.1;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 396 GATTGATGATATCTCCACTGACGTAAAGGATGACCATCCACGACTA 445
|||||
DB 104 GATTGATGATATCTCCACTGACGTAAAGGATGACCATCCACGACTA 153
|||||

Search completed: April 14, 2003, 10:25:46
Job time : 1396.64 secs

